GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 ; Search time 272 Seconds
(without alignments)
14613.151 Million cell updates/sec

Title: US-09-601-267-1
Perfect score: 1765
Sequence: 1 agctactcaggaggctgaga.....gatataacccccacaagctt 1765

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002:*
1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1765	100.0	1765	20	AAZ07247	Human telomerase R
2	1719.6	97.4	2426	19	AAV22994	DNA containing hum
3	1640.8	93.0	2425	17	AAT10283	Gene for RNA compo
4	1640.8	93.0	2425	17	AAT11027	DNA encoding the h
5	967.4	54.8	981	19	AAV41194	PstI fragment cont
6	967.4	54.8	981	19	AAV19481	Human telomerase h
7	966.4	54.8	981	24	AAD24234	Human telomerase (
8	965.8	54.7	981	18	AAT89242	Clone containing h
9	965.8	54.7	981	19	AAV63644	Human telomerase R
10	965.8	54.7	981	20	AAZ23626	Human clone 28-1 c
11	965.8	54.7	981	21	AAA37564	Human telomerase n
12	965.8	54.7	981	23	AAS15442	PstI fragment cont
13	954.4	54.1	980	22	AAS09471	Human DNA containi
14	883.4	50.1	4118	18	AAT69188	Construct pGEM-hTR
15	881.6	49.9	962	18	AAT85371	Human telomerase R
16	881.6	49.9	962	18	AAT69192	cDNA from RNA comp
17	881.6	49.9	962	19	AAV68461	Human telomerase R
18	867	49.1	867	20	AAZ07250	Human telomerase R
19	841.6	47.7	975	18	AAT69174	Standard RNA hTRKb
20	835.4	47.3	4118	18	AAT69189	Construct pGEM-hTR
21	835.2	47.3	975	18	AAT69175	Standard RNA hTRKc
22	830.4	47.0	975	18	AAT69173	Standard RNA hTRKa
23	588.6	33.3	680	18	AAT58803	Human telomerase e
24	526.4	29.8	540	19	AAV13833	Homo sapiens telom
25	526.4	29.8	540	19	AAV05373	Human telomerase p
26	523.2	29.6	540	19	AAV13838	Homo sapiens telom
27	523.2	29.6	540	19	AAV13837	Homo sapiens telom
28	523.2	29.6	540	19	AAV05374	Human telomerase p
29	521.6	29.6	540	19	AAV16092	Human telomerase p
30	509.2	28.8	538	19	AAV13839	Homo sapiens telom
31	509.2	28.8	538	19	AAV16093	Human telomerase p
32	474.6	26.9	559	17	AAT10282	RNA component of h
33	474.6	26.9	559	17	AAT11031	Human telomerase R
34	437.4	24.8	451	19	AAV41195	RNA component of h
35	437.4	24.8	451	23	AAS15919	Human telomerase (
36	437.4	24.8	451	24	ABA92070	Human telomerase R
37	424	24.0	490	21	AAA88251	Human telomerase R
38	382	21.6	448	18	AAT58802	Human telomerase R
39	367	20.8	444	21	AAA08190	Human telomerase R
40	250	14.2	590	17	AAT11028	DNA encoding the b
41	176	10.0	176	20	AAZ07323	Human telomerase R
42	176	10.0	176	20	AAZ07251	Human telomerase R
43	106	6.0	15650	22	ABA15903	Human nervous syst
44	106	6.0	15650	22	ABA16364	Human nervous syst
c 45	106	6.0	42738	22	AAK68992	Human immune/haema

ALIGNMENTS

RESULT 1
AAZ07247
ID AAZ07247 standard; DNA; 1765 BP.
XX
AC AAZ07247;
XX
DT 22-OCT-1999 (first entry)
XX
DE Human telomerase RNA (hTR) gene sequence.
XX
KW Telomerase RNA; TR; promoter; cytotoxin; cancer; neoplasia; hTR;
KW gene therapy; thymidine kinase gene; anticancer therapy; human; ss.
XX
OS Homo sapiens.
XX
PN WO9938964-A2.
XX
PD 05-AUG-1999.
XX
PF 29-JAN-1999; 99WO-GB00308.
XX
PR 29-JAN-1998; 98GB-0001902.
XX
PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX
PI Keith WN;
XX
DR WPI; 1999-479183/40.
XX
PT Mouse and human telomerase RNA gene promoters, useful for tumor
PT specific gene therapy
XX

```
PS   Disclosure; Fig 1; 109pp; English.
XX
CC   The invention relates to promoter regions from mouse and human telomerase
CC   RNA (TR) component genes. The TR gene promoter can be linked to a
CC   heterologous gene, especially a gene encoding a cytotoxin, for therapy
CC   of cancer, especially neoplasias. The telomerase is necessary for the
CC   unrestricted proliferative capacity of many human cancers. Mutation or
CC   dysregulation of the telomerase repression pathway may cause reactivation
CC   or upregulation of telomerase expression in cancer. Substances,
CC   identified in the methods, can be used to block transcription from the TR
CC   gene promoter through interaction of the 5' regulatory sequences. These
CC   substances, e.g. antisense oligonucleotides, transcription factors,
CC   peptide nucleic acids and factors that disrupt signal transduction, are
CC   useful for cancer therapy. In particular, gene therapy vectors
CC   (especially pGT62-codAupp) comprising the promoter and a viral thymidine
CC   kinase gene can be used to convert a prodrug, e.g. gancyclovir, so that
CC   neoplasia can be controlled or treated. Direct down-regulation of
CC   telomerase RNA gene through manipulation of transcription factors may be
CC   effective anticancer therapy and the cloning of the hTR gene promoter
CC   allows the analysis of therapeutic molecules which modulate hTR promoter
CC   activity. The present sequence represents a human TR (hTR) gene sequence.
XX
SQ   Sequence 1765 BP; 404 A; 458 C; 480 G; 423 T; 0 other;

  Query Match             100.0%;  Score 1765;  DB 20;  Length 1765;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1765;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
Db       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
Db      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
Db     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
Db     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
Db     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
Db     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
Db     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420

Qy     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
Db     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
Db     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
Db     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
Db     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
Db     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
Db     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
Db     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
Db     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
Db     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960

Qy     961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
Db     961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
Db    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080

Qy    1081 GCACCTACTGCCACCGCGAAGAGTTGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGG 1140
Db    1081 GCACCTACTGCCACCGCGAAGAGTTGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGG 1140

Qy    1141 CGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGC 1200
Db    1141 CGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGC 1200

Qy    1201 GATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCC 1260
Db    1201 GATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCC 1260

Qy    1261 TGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTT 1320
Db    1261 TGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTT 1320

Qy    1321 GTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAG 1380
Db    1321 GTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAG 1380

Qy    1381 GCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCC 1440
Db    1381 GCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCC 1440

Qy    1441 TGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGT 1500
Db    1441 TGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGT 1500

Qy    1501 TCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCC 1560
Db    1501 TCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCC 1560

Qy    1561 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGA 1620
Db    1561 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGA 1620

Qy    1621 ATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGT 1680
Db    1621 ATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGT 1680

Qy    1681 TTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGC 1740
Db    1681 TTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGC 1740

Qy    1741 AGTAGGATATAACCCCCACAAGCTT 1765
```

```
Db   1741 AGTAGGATATAACCCCCACAAGCTT 1765


RESULT 2
AAV22994
ID   AAV22994 standard; DNA; 2426 BP.
XX
AC   AAV22994;
XX
DT   30-JUL-1998  (first entry)
XX
DE   DNA containing human telomerase RNA component gene sequences.
XX
KW   Human; telomerase RNA component gene sequence;
KW   ribonucleoprotein enzyme; cancer cell; telomerase activity;
KW   reporter construct; transcription regulatory region;
KW   prophylaxis; therapy; telomerase-related condition;
KW   chromatin position effect; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   TATA_signal     1438..1444
FT                   /*tag= a
FT   misc_feature    1238..1259
FT                   /*tag= b
FT                   /note= "PSE consensus sequence"
FT   misc_feature    1406..1414
FT                   /*tag= c
FT                   /note= "PSE consensus sequence"
FT   CAAT_signal     1399..1406
FT                   /*tag= d
FT   misc_feature    1354..1359
FT                   /*tag= e
FT                   /note= "SP1 consensus sequence"
FT   misc_feature    1234..1245
FT                   /*tag= f
FT                   /note= "beta-interferon response element"
XX
PN   WO9811207-A2.
XX
PD   19-MAR-1998.
XX
PF   16-SEP-1997;   97WO-US16450.
XX
PR   16-SEP-1996;   96US-0714482.
XX
PA   (GERO-) GERON CORP.
XX
PI   Harley C,  Villeponteau B;
XX
DR   WPI; 1998-207376/18.
XX
PT   Human telomerase reporter constructs - useful in assays for
PT   regulators of mammalian telomerase expression
XX
PS   Claim 6; Pages 27-28; 59pp; English.
XX
CC   The present sequence contains human telomerase RNA component gene
CC   sequences. Telomerase is a ribonucleoprotein enzyme that synthesises
CC   one strand of the telomeric DNA using as a template a sequence contained
CC   within the RNA component of the enzyme. Most cancer cells express high
CC   levels of telomerase activity, while in normal somatic human cells,
CC   telomerase is not detected. The specification describes the production
CC   of a telomerase reporter construct which comprises a recombinant
CC   polynucleotide having a transcription regulatory region of a telomerase
CC   gene operably linked to a nucleotide sequence encoding a reporter
CC   polynucleotide heterologous to the transcription regulatory region.
CC   Expression of the reporter polynucleotide is detectable. The telomerase
CC   reporter construct is used in screening assays for determining modulators
CC   of transcription. The modulators can be used for prophylaxis or therapy
CC   of telomerase-related conditions. The reporter construct which has a
CC   selectable drug marker can be used to generate position effect reporter
CC   cells which can be used to determine whether a test agent inhibits
CC   chromatin position effect. Tagged RNA component constructs can be used
CC   to determine whether an agent modulates association between a mammalian
CC   RNA telomerase component and a mammalian telomerase.
XX
SQ   Sequence 2426 BP; 620 A; 575 C; 650 G; 581 T; 0 other;

  Query Match             97.4%;  Score 1719.6;  DB 19;  Length 2426;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 1750;  Conservative    0;  Mismatches   14;  Indels    2;  Gaps    2;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
           |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db     961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy     421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy     961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy    1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
           ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy    1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGACGAGTCCCCGCGCGCGGCG 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy    1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy    1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy    1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy    1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy    1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy    1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy    1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
           ||   |  |||  ||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy    1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy    1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy    1740 CAGTAGGATATAACCCCCACAAGCTT 1765
           |||||||||||||||||||||||||
Db    2401 CAGTAGGATATAACCCCCACAAGCTT 2426
```

RESULT 3
AAT10283
ID AAT10283 standard; DNA; 2425 BP.
XX
AC AAT10283;
XX
DT 09-SEP-1996 (first entry)
XX
DE Gene for RNA component of human telomerase.
XX
KW RNA component; human; telomerase; lung fibroblast; cell line WI-38;
KW recombinant production; synthesis; mutant; detection; mammalian;
KW identification; modulating agent; neoplastic condition; gene;
KW transcriptional regulatory sequence; gene therapy; disease; ss.
XX
OS Homo sapiens.
XX
PN WO9601835-A1.
XX
PD 25-JAN-1996.
XX
PF 06-JUL-1995; 95WO-US08530.
XX
PR 07-JUN-1995; 95US-0482115.
PR 07-JUL-1994; 94US-0272102.
PR 27-OCT-1994; 94US-0330123.
PR 07-JUN-1995; 95US-0472802.
XX
PA (GERO-) GERON CORP.
XX
PI Andrews WH, Feng J, Funk W, Villeponteau B;
XX
DR WPI; 1996-097581/10.
XX
PT RNA component of mammalian telomerase, esp. human - useful in
PT identifying e.g. candidate telomerase-modulating agents
XX
PS Claim 14; Pages 97-98; 114pp; English.
XX
CC The present sequence is the gene for the RNA component of human
CC telomerase (RCHT), which was derived from a genomic DNA library
CC obtd. from the human lung fibroblast cell line WI-38. The gene
CC and the RCHT can be used in the recombinant prodn. of an active
CC telomerase mol., capable of adding sequences to chromosomal DNA
CC telomeres, and in the synthesis of mutant sequences for the
CC detection of mutant mammalian telomerase RNA component
CC polynucleotides. The RCHT may also be used in the identification
CC of telomerase modulating agents, and in the detection of
CC telomerase related, or neoplastic conditions in a patient.
CC Polynucleotides of at least 25 consecutive nucleotides identical,
CC or complementary to the RCHT sequence linked to heterologous
CC transcriptional regulatory sequences, can be used for the gene
CC therapy of human diseases.
XX
SQ Sequence 2425 BP; 622 A; 572 C; 650 G; 581 T; 0 other;

Query Match 93.0%; Score 1640.8; DB 17; Length 2425;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1742; Conservative 0; Mismatches 17; Indels 11; Gaps 8;

```
Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
           |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db     961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080
```

```
Qy    421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy    481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy    541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy    601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy    661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy    721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy    781 CTCGCCCGGCAGCGCACCGGGTTGC----GGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 836
          ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db   1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 1500

Qy    837 TTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTG 896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTG 1560

Qy    897 TTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCAT 956
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCAT 1620

Qy    957 TCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGC 1016
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1621 TCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCC-GGGACCTGCGGC 1679

Qy    1017 GGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCC 1076
           |||||| |||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1680 GGGTCG-CTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGG-CCGGGGCTTCTCC 1737

Qy    1077 GGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGC 1135
           |||||||| |||||||||||||||||| ||||||||||||||||||||||||||||||
Db   1738 GGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGC 1797

Qy    1136 GAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGC 1195
           |||||||||||||  | |||||||||||||||||||||||||||||| ||||||||
Db   1798 GAGGGCGAGGTTCA-CCGTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGT-CCCGCGCGC 1855

Qy    1196 GGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGC 1255
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db   1856 GGCGCGATTCCCTGAGCTATGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGC 1915

Qy    1256 TTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGG 1315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1916 TTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGG 1975

Qy    1316 GGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACG 1375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1976 GGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACG 2035

Qy    1376 TGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCC 1435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2036 TGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCC 2095

Qy    1436 GTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAAC 1495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2096 GTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAAC 2155

Qy    1496 TTAGTTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACC 1555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2156 TTAGTTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACC 2215

Qy    1556 AGTCCCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTT 1615
           ||||||    |  |||    ||||||||||||||||||||||||||||||||||||||||
Db   2216 AGTCCCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTT 2275

Qy    1616 AATGAATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCA 1675
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2276 AATGAATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCA 2335

Qy    1676 TCGGTTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCT 1735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2336 TCGGTTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCT 2395

Qy    1736 TGAGCAGTAGGATATAACCCCCACAAGCTT 1765
           |||||||||||||||||||||||||||||
Db   2396 TGAGCAGTAGGATATAACCCCCACAAGCTT 2425
```

RESULT 4
AAT11027
ID AAT11027 standard; DNA; 2425 BP.
XX
AC AAT11027;
XX
DT 09-JUN-1996 (first entry)
XX
DE DNA encoding the human telomerase RNA component.
XX
KW Telomerase; mammal; antisense; triplex forming oligonucleotide;
KW plasmid; probe; primer; ribozyme; ss.
XX
OS Homo sapiens.
XX
PN WO9601614-A2.
XX
PD 25-JAN-1996.
XX
PF 07-JUL-1995; 95WO-US08620.
XX
PR 07-JUN-1995; 95US-0485778.
PR 07-JUL-1994; 94US-0272102.
PR 27-OCT-1994; 94US-0330123.
PR 13-FEB-1995; 95US-0387524.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
PA (GERO-) GERON CORP.
XX
PI Andrews WH, Avillon AA, Feng J, Funk W, Greider C;
PI Marhuenda MA, Villeponteau B;
XX
DR WPI; 1996-097428/10.
XX
PT RNA components of (non)human mammalian telomerase(s) - useful in
PT studying cell senescence and immortalisation
XX
PS Claim 37; Figure 1; 85pp; English.
XX
CC The RNA components of (non) human mammalian telomerase(s) especially
CC from mouse, rat and chinese hamster are all claimed. Antisense
CC oligonucleotides can be used to block the activity of the
CC telomerase; probes and primers can be used in detection; vectors and
CC host cells transformed with the isolated telomerase genes can be
CC used for production of telomerases; RNA and DNA ribozymes and triplex
CC forming oligonucleotides directed against the telomerase genes can
CC be used therapeutically as can plasmids. A mouse which lacks the
CC telomerase gene (also claimed) can be used for study of telomere
CC regulation in vivo, and the role it plays in immortalisation. This
CC DNA sequence encodes the human telomerase RNA component.
XX
SQ Sequence 2425 BP; 622 A; 572 C; 650 G; 581 T; 0 other;

```
  Query Match             93.0%;  Score 1640.8;  DB 17;  Length 2425;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 1742;  Conservative    0;  Mismatches   17;  Indels   11;  Gaps    8;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
           |||||| ||||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db     961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy     421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGC----GGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 836
           |||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db    1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 1500

Qy     837 TTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTG 896
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTG 1560

Qy     897 TTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCAT 956
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 TTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCAT 1620

Qy     957 TCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGC 1016
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    1621 TCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCC-GGGACCTGCGGC 1679

Qy    1017 GGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCC 1076
           |||||| |||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    1680 GGGTCG-CTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGG-CCGGGGCTTCTCC 1737

Qy    1077 GGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGC 1135
           |||||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||
Db    1738 GGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGC 1797

Qy    1136 GAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGC 1195
           |||||||||||||  | ||||||||||||||||||||||||||||| |||||||||
Db    1798 GAGGGCGAGGTTCA-CCGTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGT-CCCGCGCGC 1855

Qy    1196 GGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGC 1255
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    1856 GGCGCGATTCCCTGAGCTATGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGC 1915

Qy    1256 TTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGG 1315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1916 TTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGG 1975

Qy    1316 GGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACG 1375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1976 GGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACG 2035

Qy    1376 TGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCC 1435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2036 TGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCC 2095

Qy    1436 GTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAAC 1495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2096 GTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAAC 2155

Qy    1496 TTAGTTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACC 1555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2156 TTAGTTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACC 2215

Qy    1556 AGTCCCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTT 1615
           ||||||   |  |||   ||||||||||||||||||||||||||||||||||||||||||
Db    2216 AGTCCCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTT 2275

Qy    1616 AATGAATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCA 1675
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2276 AATGAATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCA 2335

Qy    1676 TCGGTTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCT 1735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2336 TCGGTTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCT 2395

Qy    1736 TGAGCAGTAGGATATAACCCCCACAAGCTT 1765
           |||||||||||||||||||||||||||||||
Db    2396 TGAGCAGTAGGATATAACCCCCACAAGCTT 2425


RESULT 5
AAV41194
ID   AAV41194 standard; DNA; 981 BP.
XX
AC   AAV41194;
XX
DT   08-OCT-1998  (first entry)
XX
DE   PstI fragment containing RNA component of human telomerase (hTR).
XX
KW   RNA component; human telomerase; antisense oligonucleotide; infection;
KW   neuroblastoma; bladder cancer; colon cancer; prostate cancer; cancer;
KW   contraception; sterilisation; immunosuppression; therapeutic; hTR;
KW   immune system down-regulation; anti-inflammatory therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    266..716
FT                   /*tag=  a
```

```
FT                   /note= "RNA component of human telomerase (hTR)"
FT   misc_feature    311..320
FT                   /*tag=  b
FT                   /note= "template region of hTR"
XX
PN   WO9828442-A1.
XX
PD   02-JUL-1998.
XX
PF   19-DEC-1997;   97WO-US23619.
XX
PR   20-DEC-1996;   96US-0770565.
PR   20-DEC-1996;   96US-0770564.
XX
PA   (GERO-) GERON CORP.
XX
PI   Kealey JT,  Kim NW,  Pruzan R,  Weinrich SL,  Wu F;
XX
DR   WPI; 1998-377670/32.
XX
PT   New polynucleotide(s) anti:sense to human telomerase - used for
PT   detecting or inhibiting human telomerase, e.g. for treating cancers,
PT   contraception, immuno-suppression or treating infection
XX
PS   Disclosure; Page 53; 80pp; English.
XX
CC   This represents a PstI fragment containing the RNA component of human
CC   telomerase (hTR). The invention provides antisense oligonucleotides
CC   (AAV41169 to AAV41181) to hTR. These antisense oligonucleotides
CC   specifically hybridise to a nucleotide sequence within an accessible
CC   region of the hTR, but that does not hybridise to a sequence within the
CC   template region of hTR. These oligonucleotides may specifically be used
CC   for detection of an RNA component of human telomerase in a sample. This
CC   is useful for diagnosing cancer (especially neuroblastoma, bladder, colon
CC   and prostate cancer), and providing prognosis for a cancer patient. The
CC   inhibitory oligonucleotides can inhibit the telomerase activity level in
CC   a cell by interfering with transcription of the RNA component, decreasing
CC   the half-life of the telomerase RNA component transcript, inhibiting
CC   assembly of the RNA component into the telomerase holoenzyme, or
CC   inhibiting the polymerase activity of telomerase. These antisense
CC   oligonucleotides can be used for inhibiting telomerase activity in both
CC   cultured cells and in cells in vivo. They can be used in therapeutics for
CC   treating or preventing cancer, for contraception or sterilisation, for
CC   immunosuppression, and for selectively down-regulating specific branches
CC   of the immune system, e.g. a specific subset of T-cells, in anti-
CC   inflammatory therapies or for treating infections by, e.g. yeast,
CC   parasites or fungi.
XX
SQ   Sequence 981 BP; 172 A; 303 C; 306 G; 200 T; 0 other;

  Query Match             54.8%;  Score 967.4;  DB 19;  Length 981;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-261;
  Matches  979;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CATTCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy    1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy    1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
           |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db     541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy    1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy    1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy    1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy    1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy    1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy    1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy    1493 AACTTAGTTCCTGCTCTGCAG 1513
           |||||||||||||||||||||
Db     961 AACTTAGTTCCTGCTCTGCAG 981
```

```
RESULT 6
AAV19481
ID   AAV19481 standard; cDNA; 981 BP.
XX
AC   AAV19481;
XX
DT   28-AUG-1998  (first entry)
XX
DE   Human telomerase hTR gene.
XX
KW   Telomerase; hTR gene; TPC2; TPC3; telomere length; human; cancer;
KW   gene therapy; diagnosis; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   unsure          21
FT                   /*tag=  a
FT   mRNA            266..715
FT                   /*tag=  b
XX
PN   WO9811204-A1.
XX
```

```
PD   19-MAR-1998.
XX
PF   13-SEP-1996;   96WO-US14679.
XX
PR   13-SEP-1996;   96WO-US14679.
XX
PA   (GERO-) GERON CORP.
XX
PI   Adams RR,  Andrews WH,  Feng J,  Villeponteau B;
XX
DR   WPI; 1998-207373/18.
XX
PT   Human TPC2, TPC3 and TR genes - regulate telomere length or modulate
PT   telomerase activity
XX
PS   Disclosure; Fig 9A-B; 86pp; English.
XX
CC   This nucleotide sequence comprises an approximately 1 kb PstI
CC   restriction fragment of plasmid pGRN33 that includes the human
CC   telomerase hTR gene.  hTR3 mRNA levels correlate with telomerase
CC   activity levels in a variety or mortal and immortal cell lines.
CC   In methods of the invention, measurements of telomere length,
CC   telomerase activity or hTR levels can be used to identify immortal
CC   cells, such as cancer cells, and to evaluate the proliferative
CC   capacity of the cell.  Gene therapy vectors encode useful nucleic
CC   acids such as hTR, or antisense nucleic acids or ribozymes that
CC   target TPC2, TPC3 (see AAV19479-80) and/or hTR gene products.
XX
SQ   Sequence 981 BP; 172 A; 303 C; 306 G; 200 T; 0 other;

  Query Match             54.8%;  Score 967.4;  DB 19;  Length 981;
  Best Local Similarity   99.8%;  Pred. No. 1.3e-261;
  Matches  979;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy    1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy    1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
           |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db     541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy    1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy    1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy    1253 CGCTTTCCTGTTGGTGGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGCTTTCCTGTTGGTGGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy    1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy    1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy    1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy    1493 AACTTAGTTCCTGCTCTGCAG 1513
           |||||||||||||||||||||
Db     961 AACTTAGTTCCTGCTCTGCAG 981


RESULT 7
AAD24234
ID   AAD24234 standard; DNA; 981 BP.
XX
AC   AAD24234;
XX
DT   07-MAR-2002  (first entry)
XX
DE   Human telomerase (hTR) gene.
XX
KW   Human; telomerase; TR; telomerase activity-related disease; therapy;
KW   cancer; pregnancy; fertility; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    267..715
FT                   /*tag= a
FT                   /note= "hTR transcript serves as template in the
FT                   telomerase ribonucleoprotein"
XX
PN   US6300110-B1.
XX
PD   09-OCT-2001.
XX
PF   23-DEC-1998;   98US-0220157.
XX
PR   09-SEP-1995;   95US-003492P.
PR   13-SEP-1996;   96US-0710249.
PR   05-JAN-1996;   96US-0583808.
XX
PA   (GERO-) GERON CORP.
XX
PI   Villeponteau B,  Feng J,  Andrews WH,  Adams RR;
XX
DR   WPI; 2002-033174/04.
XX
PT   Peptide products of the human TPC2 and TPC3 gene are involved in
PT   regulation of telomere length and activity are useful to diagnose and
PT   treat telomere length and activity-related diseases -
XX
PS   Example; Fig 9; 60pp; English.
XX
```

```
CC   The invention relates to methods and reagents for regulating telomere
CC   length and for modulating telomerase activity in mammalian cells. The
CC   invention also relates to purified, synthetic or recombinant peptides
CC   such as TPC2 or TPC3 used for detecting regulators of telomere length
CC   and telomerase activity in mammalian cells and for a variety of related
CC   diagnostic and therapeutic purposes. The method is useful for screening,
CC   diagnosing, monitoring and treating diseases and other conditions such as
CC   cancer, pregnancy, fertility, telomere length and telomerase-activity.
CC   The present sequence is human telomerase (hTR) gene.
XX
SQ   Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

  Query Match            54.8%;  Score 966.4;  DB 24;  Length 981;
  Best Local Similarity  99.7%;  Pred. No. 2.5e-261;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGNCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CATTCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy    1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy    1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
           |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db     541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy    1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy    1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy    1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy    1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy    1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy    1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy    1493 AACTTAGTTCCTGCTCTGCAG 1513
           |||||||||||||||||||||
Db     961 AACTTAGTTCCTGCTCTGCAG 981


RESULT 8
AAT89242
ID   AAT89242 standard; DNA; 981 BP.
XX
AC   AAT89242;
XX
DT   12-MAY-1998  (first entry)
XX
DE   Clone containing hTR sequence.
XX
KW   Peptide nucleic acid; PNA; cancer; telomerase; probe; hybridisation;
KW   inhibitor; human telomerase RNA; hTR; ds.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 265..716
FT                   /*tag= a
FT                   /note= "human telomerase RNA"
XX
PN   WO9738013-A1.
XX
PD   16-OCT-1997.
XX
PF   09-APR-1997;   97WO-US05931.
XX
PR   09-APR-1996;   96US-0630019.
XX
PA   (GERO-) GERON CORP.
XX
PI   Corey D,  Norton JC,  Piatyszek MA,  Shay JW,  Wright WE;
XX
DR   WPI; 1997-512647/47.
XX
PT   New peptide nucleic acids hybridising to mammalian telomerase RNA -
PT   used to inhibit telomerase, for treating tumours and other
PT   proliferative diseases, also for diagnosis
XX
PS   Disclosure; Pages 20-21; 76pp; English.
XX
CC   This fragment of cloned DNA contains the human telomerase RNA (hTR)
CC   sequence, (266-716bp). The hTR region contains a CCC template which
CC   the peptide nucleic acid (PNA) can recognise.  The presence of a GGG
CC   in the PNAs allows for the specific hybridisation to the template
CC   region of this hTR component.  PNAs can be used as probes to detect the
CC   RNA component of mammalian telomerase and as inhibitors of telomerase
CC   activity, especially in the treatment of cancer.
XX
SQ   Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

  Query Match            54.7%;  Score 965.8;  DB 18;  Length 981;
  Best Local Similarity  99.7%;  Pred. No. 3.6e-261;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy    1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy    1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
           |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||||
Db     541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy    1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy    1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy    1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy    1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy    1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy    1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy    1493 AACTTAGTTCCTGCTCTGCAG 1513
           |||||||||||||||||||||
Db     961 AACTTAGTTCCTGCTCTGCAG 981


RESULT 9
AAV63644
ID   AAV63644 standard; DNA; 981 BP.
XX
AC   AAV63644;
XX
DT   15-FEB-1999  (first entry)
XX
DE   Human telomerase RNA component sequence from lambda clone 28-1.
XX
KW   Lambda clone 28-1; human; telomerase RNA component; anticancer therapy;
KW   assay; vaccine; cancer; purification; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    266..716
FT                   /*tag=  a
FT                   /note= "human telomerase RNA component sequence"
XX
PN   WO9845450-A1.
XX
PD   15-OCT-1998.
XX
PF   04-APR-1997;   97WO-US06012.
XX
PR   04-APR-1997;   97WO-US06012.
XX
PA   (GERO-) GERON CORP.
XX
PI   Atkinson EM,  Kealey JT,  Lichtsteiner SP,  Pruzan RA;
PI   Vasserot AP,  Weinrich SL;
XX
DR   WPI; 1998-594485/50.
XX
PT   Purification of telomerase on affinity material  - useful for, e.g.
PT   diagnosis and treatment of cancer
XX
PS   Disclosure; Pages 14-15; 76pp; English.
XX
CC   The present sequence represents the PstI fragment of the 2.4 kb
CC   SauIIIA1-HindIII fragment of lambda clone 28-1. This clone contains
CC   human telomerase RNA component gene sequences. The specification
CC   provides methods for purifying human telomerase. The methods involve
CC   the use of several sequential steps; including the use of two matrixes
CC   that bind molecules bearing negative charges, a matrix that binds
CC   molecules bearing positive charges, an affinity purification step
CC   and a size separation. Telomerase is a particular target of anticancer
CC   therapies, and is useful in assays for characterizing (pre)cancerous
CC   cells. The present sequence can be used for such assays. Telomerase can
CC   also be used to screen for specific modulators, for biochemical analysis
CC   of its activity, and in preparation of antibodies. Fragments of
CC   telomerase, or nucleic acid encoding them, are used in vaccines, and
CC   for treating over expression of telomerase, particularly in cancer.
XX
SQ   Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

  Query Match           54.7%;  Score 965.8;  DB 19;  Length 981;
  Best Local Similarity  99.7%;  Pred. No. 3.6e-261;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
```

```
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CATTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy        894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy        954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy       1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy       1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
              |||||||||||| ||||||||||||||||||| |||||||||||||||||||||||||||
Db        541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy       1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy       1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy       1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy       1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy       1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy       1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy       1493 AACTTAGTTCCTGCTCTGCAG 1513
              |||||||||||||||||||||
Db        961 AACTTAGTTCCTGCTCTGCAG 981


RESULT 10
AAZ23626
ID   AAZ23626 standard; DNA; 981 BP.
XX
AC   AAZ23626;
XX
DT   07-JAN-2000  (first entry)
XX
DE   Human clone 28-1 containing telomerase fragment.
XX
KW   Telomerase; human; immune response; cancer; vaccine; treatment;
KW   disease; ss.
XX
OS   Homo sapiens.
XX
PN   US5968506-A.
XX
PD   19-OCT-1999.
XX
PF   04-APR-1997;   97US-0833377.
XX
PR   04-AUG-1995;   95US-0510736.
XX
PA   (GERO-) GERON CORP.
XX
PI   Atkinson EM,  Lichtsteiner SP,  Weinrich SL,  Pruzan RA,  Kealey JT;
PI   Vasserot AP;
XX
DR   WPI; 1999-590379/50.
XX
PT   Compositions comprising human telomerase, useful for treating diseases
PT   associated with overexpression of telomerase e.g. cancer -
XX
PS   Disclosure; Column 41-42; 34pp; English.
XX
CC   This invention describes a novel composition comprising human telomerase
CC   having at least 2000-fold (preferably at least 60000-fold) increased
CC   relative purity compared with crude extract of cells from
CC   adenovirus-transformed kidney cell line. The composition is useful for
CC   eliciting an immune response in animals and may therefore be used as a
CC   vaccine for treating diseases associated with the overexpression of
CC   telomerase e.g. cancer. This sequence represents a nucleic acid fragment
CC   from human clone 28-1 which contains a fragment of the human telomerase
CC   described in the method of the invention.
XX
SQ   Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

  Query Match             54.7%;  Score 965.8;  DB 20;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 3.6e-261;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy        534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db          1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy        594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy        654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy        714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy        774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy        834 CATTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CATTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy        894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy        954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy       1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy       1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
              |||||||||||| ||||||||||||||||||| |||||||||||||||||||||||||||
Db        541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy       1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy       1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720
```

```
Qy   1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy   1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy   1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy   1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy   1493 AACTTAGTTCCTGCTCTGCAG 1513
          |||||||||||||||||||||
Db    961 AACTTAGTTCCTGCTCTGCAG 981
```

RESULT 11
AAA37564
ID AAA37564 standard; DNA; 981 BP.
XX
AC AAA37564;
XX
DT 15-AUG-2000 (first entry)
XX
DE Human telomerase nucleotide sequence.
XX
KW Peptide nucleic acid; PNA; telomerase; ribonucleoprotein enzyme; cancer;
KW inhibitor; neoplasia; neurodegenerative disease; aging; hyperplasia;
KW AIDS; HIV; fungal infection; forensic identification; detect; tumour;
KW paternity testing; ds.
XX
OS Homo sapiens.
XX
PN US6046307-A.
XX
PD 04-APR-2000.
XX
PF 09-APR-1997; 97US-0838545.
XX
PR 09-APR-1996; 96US-0630019.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Wright WE, Piatyszek MA, Shay JW, Norton JC, Corey DR;
XX
DR WPI; 2000-292432/25.
XX
PT New peptide nucleic acid (PNA) compounds that inhibit telomerase
PT activity in mammalian cells is useful as probes to detect the RNA
PT component of a mammalian telomerase -
XX
PS Disclosure; Column 13-14; 45pp; English.
XX
CC The present sequence represents the human telomerase nucleotide sequence.
CC The invention relates to peptide nucleic acid molecules which hybridise
CC to the mRNA component of mammalian telomerase, and inhibit telomerase
CC activity. Telomerase is a ribonucleoprotein enzyme that synthesizes one
CC strand of the telomeric DNA, using as a template an 11 nucleotide
CC sequence contained within the RNA component of the enzyme. The invention
CC relates to PNA molecules having a sequence of no more than 25 bases,
CC which include the sequence GTTAGG. The uncharged nature of the PNA
CC backbone increases the melting temperature of associating strands,
CC increases the rate of association with targeted nucleic acids, and
CC affords greater resistance of degradation by proteases or nucleases. The
CC therapeutic PNAs may be used for treating disease conditions such as
CC cancers, neoplasia, hyperplasia, neurodegenerative diseases, aging, human
CC immunodeficiency virus (HIV) infection/AIDS (acquired immunodeficiency
CC syndrome) and associated pathologies, fungal infections, and other
CC diseases characterized by abnormal telomere metabolism or telomerase
CC activity, in combination with antineoplastic and other cytotoxic or
CC cytostatic agents, antifungal agents, and other nucleotides. PNAs may be
CC used for molecular diagnostics, labelled PNAs are used as hybridization
CC probes to detect or quantitate polynucleotides having a human telomerase
CC RNA (hTR) sequence. PNA probes are also used for forensic identification
CC of individuals, e.g. paternity testing, based on hTR gene restriction
CC fragment length polymorphism (RFLP) pattern. PNAs are also useful as
CC probes to detect the RNA component of a mammalian telomerase and as
CC inhibitors of telomerase activity. The method of the present invention
CC allows cancerous conditions to be detected with increased confidence and
CC possibly at an earlier stage, before cells are detected as cancerous
CC based on pathological characteristics. The diagnostic and prognostic
CC methods of the present invention can be used to detect an immortal or
CC neoplastic cell or tumour tissue or cancer of any origin, provided the
CC cell expresses telomerase activity and its RNA component.
XX
SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 54.7%; Score 965.8; DB 21; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.6e-261;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy    534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
          |||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db      1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy    594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy    654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy    714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy    774 AAGCCGACTCGCCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy    834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy    894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy    954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy   1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy   1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
          |||||||||||  |||||||||||||||||| ||||||||||||||||||||||||||||
Db    541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy   1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy   1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy   1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy   1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy   1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy   1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy   1493 AACTTAGTTCCTGCTCTGCAG 1513
          |||||||||||||||||||||
Db    961 AACTTAGTTCCTGCTCTGCAG 981
```

RESULT 12
AAS15442
ID AAS15442 standard; DNA; 981 BP.
XX
AC AAS15442;
XX
DT 14-FEB-2002 (first entry)
XX
DE PstI fragment containing human telomerase RNA component gene sequence.
XX
KW Mammalian; forensic; paternity testing; human telomerase RNA component;
KW hTR gene RFLP pattern; cancer; inflammation; lymphoproliferative disease;
KW autoimmune disease; neurodegenerative disease; neoplasia; hyperplasia;
KW HIV; AIDS; human immunodeficiency virus; telomere metabolism; cytostatic;
KW acquired immunodeficiency syndrome; anti-inflammatory; immunosuppressive;
KW bacteriophage lambda clone 28-1; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 266..716
FT /*tag= a
FT /note= "htr gene sequence"
FT misc_feature 311..320
FT /*tag= b
FT /note= "Template region of hTR used as template for
FT synthesis of telomeric repeats"
XX
PN US6294650-B1.
XX
PD 25-SEP-2001.
XX
PF 08-JUL-1999; 99US-0349532.
XX
PR 09-APR-1997; 97US-0838545.
PR 09-APR-1996; 96US-0630019.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Shay JW, Wright WE, Piatyszek MA, Corey DR, Norton JC;
XX
DR WPI; 2001-638024/73.
XX
PT New peptide nucleic acids that hybridises to the RNA component of
PT mammalian telomerase, useful for treating or preventing cancer,
PT inflammation, lymphoproliferative diseases, autoimmune disease, or
PT neurodegenerative diseases -
XX
PS Disclosure; Column 13-16; 46pp; English.
XX
CC The present invention relates to peptide nucleic acids (PNAs), comprising
CC a sequence of 6-25 nucleobases, that inhibit telomerase activity in
CC mammalian cells by hybridising to the RNA component of mammalian
CC telomerase. The PNAs are useful as probes to detect the RNA component
CC of mammalian telomerase and as inhibitors of telomerase activity, or to
CC detect and/or quantitate polynucleotide having the human telomerase
CC RNA component (hTR) sequence, as well as in forensic identification of
CC individuals, such as paternity testing or identification of criminal
CC suspects or unknown descendants based on the hTR gene RFLP pattern. The
CC PNA can be further used for treating or preventing cancer, inflammation,
CC lymphoproliferative diseases, autoimmune disease, or neurodegenerative
CC diseases. The PNAs in combination with other pharmaceuticals (such as
CC antineoplastic or cytostatic agents) can be used for treating neoplasia,
CC hyperplasia, human immunodeficiency virus (HIV) infections, acquired
CC immunodeficiency syndrome (AIDS) and associated pathologies, and other
CC diseases characterised by abnormal telomere metabolism or telomerase
CC activity. The present sequence represents a PstI fragment, derived
CC from bacteriophage lambda clone 28-1, containing the hTR gene sequence.
XX
SQ Sequence 981 BP; 172 A; 303 C; 305 G; 200 T; 1 other;

Query Match 54.7%; Score 965.8; DB 23; Length 981;
Best Local Similarity 99.7%; Pred. No. 3.6e-261;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy    534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
          |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy    594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy    654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy    714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy    774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy    834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy    894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy    954 CATTCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CATTCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy   1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy   1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
          |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||||
Db    541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy   1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy   1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy   1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780
```

```
Qy    1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy    1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy    1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy    1493 AACTTAGTTCCTGCTCTGCAG 1513
           |||||||||||||||||||||
Db     961 AACTTAGTTCCTGCTCTGCAG 981
```

RESULT 13
AAS09471
ID AAS09471 standard; DNA; 980 BP.
XX
AC AAS09471;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human DNA containing the RNA component of telomerase.
XX
KW Human; Telomerase; RNA component; vaccine; antibody; cancer; EF2H;
KW nucleolin; ds.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT misc_feature   21
FT   /*tag= a
FT   /note= "Designated 0 in the specification, with 7
FT   in the complementary strand"
FT misc_feature   311..320
FT   /*tag= b
FT   /label= "Template_region"
FT   /note= "This region is not further defined in the
FT   specification"
XX
PN US6261556-B1.
XX
PD 17-JUL-2001.
XX
PF 18-OCT-1999; 99US-0420056.
XX
PR 04-APR-1997; 97US-0833377.
PR 04-AUG-1995; 95US-0510736.
XX
PA (GERO-) GERON CORP.
XX
PI Weinrich SL, Atkinson EM, Lichtsteiner SP, Vasserot AP, Pruzan RA;
PI Kealey JT;
XX
DR WPI; 2001-450477/48.
XX
PT Purified human telomerase, useful for inducing immune response in
PT animals, comprises several thousand folds increased purity compared
PT with cytoplasmic crude cell preparations -
XX
PS Disclosure; Column 9-12; 29pp; English.
XX
CC The sequence contains human telomerase, hTR, RNA component. The invention
CC relates to a purified human telomerase core enzyme protein comprising
CC 2000-fold increased purity compared with a crude extract of cells from
CC adenovirus-transformed kidney cell line (293 cells) and when associated
CC with telomerase RNA component has DNA polymerase activity and a molecular
CC weight of 200-2000 kilo Daltons (kDa). The purified telomerase is useful
CC for inducing a humoral or cell-mediated immune response in an animal.
CC Purified telomerase or immunogenic fragments are useful as vaccines for
CC treating diseases associated with over-expression of telomerase, such as
CC cancer and for producing antibodies that recognize telomerase, which are
CC useful as affinity agents in isolating the proteins and for detecting the
CC presence of proteins in a sample, such as cell or tissue. Identification
CC of telomerase aids in diagnosis of cancer or pre-cancerous states.
CC Telomerase and/or telomerase associated proteins are also useful for
CC screening compounds to identify agents that alter the association of
CC telomerase-associated proteins, such as nucleolin or EF2H with
CC telomerase.
XX
SQ Sequence 980 BP; 171 A; 303 C; 305 G; 200 T; 1 other;

Query Match 54.1%; Score 954.4; DB 22; Length 980;
Best Local Similarity 99.6%; Pred. No. 5.9e-258;
Matches 977; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

```
Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGNCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db     421 CATTCTAGAGCAAAC-AAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 479

Qy    1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     480 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 539

Qy    1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
           |||||||||||| |||||||||||||||||| ||||||||||||||||||||||||||||
Db     540 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 599

Qy    1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     600 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 659

Qy    1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     660 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 719

Qy    1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     720 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 779

Qy    1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     780 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 839
```

```
Qy    1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     840 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 899

Qy    1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     900 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 959

Qy    1493 AACTTAGTTCCTGCTCTGCAG 1513
           |||||||||||||||||||||
Db     960 AACTTAGTTCCTGCTCTGCAG 980


RESULT 14
AAT69188
ID   AAT69188 standard; DNA; 4118 BP.
XX
AC   AAT69188;
XX
DT   26-FEB-1998  (first entry)
XX
DE   Construct pGEM-hTR containing RNA component of human telomerase.
XX
KW   Human telomerase; quantification; tumour cell; pGEM-hTR;
KW   detection; micrometastasis; diagnosis; lymphoblastoma; leukaemia;
KW   teratocacinoma; melanoma; carcinoma; cancer; tumour; neuroblastoma;
KW   rhabdomyosarcoma; leiomyosarcoma; lymphoma; RNA component; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    12..975
FT                   /*tag= a
FT                   /note= "cDNA from RNA component of human telomerase"
XX
PN   WO9718322-A2.
XX
PD   22-MAY-1997.
XX
PF   14-NOV-1996;   96WO-DE02183.
XX
PR   16-NOV-1995;   95DE-4042795.
XX
PA   (DAHM/) DAHM M W.
XX
PI   Dahm MW;
XX
DR   WPI; 1997-289298/26.
XX
PT   Quantifying tumour cells in body fluid - by measuring RNA component
PT   of telomerase after amplification, especially useful for early
PT   diagnosis of metastasis
XX
PS   Example 5; Fig 5; 46pp; German.
XX
CC   The present sequence is the construct pGEM-hTR, which comprises the
CC   transcription vector pGEM-13zf(+) and the cDNA from the RNA
CC   component of human telomerase. The construct was used in the
CC   development of a novel method for quantifying tumour cells in a
CC   body fluid. The method comprises specific amplification of the RNA
CC   component of telomerase, and measuring the amount of amplified
CC   nucleic acid. At least 1, preferably all 3 (AAT69173-75) standard
CC   nucleic acids are present (at different concentrations) and are
CC   co-amplified with telomerase DNA. The amplification products are
CC   detected directly or via a label or by hybridisation with a
CC   labelled oligonucleotide (AAT69184-87, 1 for each standard and 1 for
CC   telomerase), and the amount of telomerase product compared with
CC   that from the standards.
CC   The method can be used to detect tumour cells, specifically
CC   micrometastases, in a body fluid, particularly for the early
CC   diagnosis of metastatic spread and for monitoring tumour therapy.
CC   Typical tumour cells that can be quantified are micrometastases,
CC   T cell lymphoblastoma or leukaemia (chronic myelogenous, and
CC   chronic or acute lymphatic leukaemia), teratocacinoma, melanoma,
CC   carcinoma of lung, liver or prostate, cancer of colon or breast,
CC   kidney, brain or adrenal tumours, neuroblastoma, rhabdomyosarcoma,
CC   leiomyosarcoma and/or lymphoma.
XX
SQ   Sequence 4118 BP; 991 A; 1032 C; 1094 G; 1001 T; 0 other;

  Query Match             50.1%;  Score 883.4;  DB 18;  Length 4118;
  Best Local Similarity   97.6%;  Pred. No. 1.2e-237;
  Matches  950;  Conservative    0;  Mismatches   16;  Indels    7;  Gaps    5;

Qy     794 GCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAA 853
           ||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14 GCCGCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAA 73

Qy     854 CTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTT 913
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 CTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTT 133

Qy     914 CAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAA 973
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 CAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAA 193

Qy     974 ATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCC 1033
           ||||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Db     194 ATGTCAGCTGCTGGCCCGTTCG--CCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCC 251

Qy    1034 CCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTACTGCCA 1093
           |||||||||||||||| |||||||||||||||||||||||||||||||||||| ||||||
Db     252 CCCGAACCCCGCCTGGA-GCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCCACTGCCA 310

Qy    1094 CCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGC 1152
           |||||||||||| |||||||||||||||||||||||||||||||||||||||||||   |
Db     311 CCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCA-CC 369

Qy    1153 CTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGC 1212
            ||||||||||||||||||||||||||||||||||||    |||||||||||||||||||
Db     370 GTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCC--GCCGCGGCGCGATTCCCTGAGC 427

Qy    1213 TGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGG 1272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     428 TGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGG 487

Qy    1273 GAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAA 1332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     488 GAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAA 547

Qy    1333 ACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAG 1392
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     548 ACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAG 607

Qy    1393 TCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCT 1452
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     608 TCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCT 667

Qy    1453 CCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCA 1512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     668 CCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCA 727

Qy    1513 GATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCCTCAACGGGGT 1572
           ||||||||||||||||||||||||||||||||||||||||||||||||   |  |||
Db     728 GATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCTCAACGGGGTG 787

Qy    1573 GTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAG 1632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     788 TGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAG 847

Qy    1633 AAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGG 1692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     848 AAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGG 907

Qy    1693 TTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAA 1752
```

```
Db    908 TTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAA 967

Qy   1753 CCCCCACAAGCTT 1765
Db    968 CCCCCACAAGCTT 980
```

RESULT 15
AAT85371
ID AAT85371 standard; DNA; 962 BP.
XX
AC AAT85371;
XX
DT 15-APR-1998 (first entry)
XX
DE Human telomerase RNA component gene.
XX
KW Telomerase gene; transgenic organism; carcinogen; neoplastic growth;
KW cell growth; cell senescence; human; ss.
XX
OS Homo sapiens.
XX
PN WO9735967-A2.
XX
PD 02-OCT-1997.
XX
PF 21-MAR-1997; 97WO-US05070.
XX
PR 28-MAR-1996; 96US-0623166.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
PA (YESH) UNIV YESHIVA EINSTEIN COLLEGE.
XX
PI DePinho RA, Greider C, Lee H, Marhuenda MAB;
XX
DR WPI; 1997-489631/45.
XX
PT Non-human transgenic animal not expressing endogenous telomerase -
PT useful to test the carcinogenicity of a test compound, or to study
PT cell growth, division or senescence
XX
PS Disclosure; Fig 5; 58pp; English.
XX
CC This sequence represents the human telomerase RNA component gene. This
CC sequence can be used in the transgenic organism of the invention. The
CC organism is a non-human transgenic organism in which at least one
CC endogenous telomerase gene encoding a telomerase component is altered and
CC telomerase activity is altered or is not expressed. The transgenic
CC organisms can be used as models to study telomerase activity. They can
CC also be used as a system to test compounds suspected of being
CC carcinogenic by exposing animals to the compound and determining
CC neoplastic growth as an indicator of carcinogenicity. The cells and
CC derived tissues are used to study cell growth and division and cell
CC senescence. The organisms are able to produce cells and tissues that, in
CC their wild type form, cannot be easily studied in vitro due to undergoing
CC small numbers of cell divisions.
XX
SQ Sequence 962 BP; 178 A; 257 C; 288 G; 239 T; 0 other;

Query Match 49.9%; Score 881.6; DB 18; Length 962;
Best Local Similarity 97.8%; Pred. No. 1.8e-237;
Matches 947; Conservative 0; Mismatches 14; Indels 7; Gaps 5;

```
Qy    799 GGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAACTGAG 858
Db      1 GGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAACTGAG 60

Qy    859 AAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTTCAGCG 918
Db     61 AAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTTCAGCG 120

Qy    919 GGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAAATGTC 978
Db    121 GGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAAATGTC 180

Qy    979 AGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCCCCCGA 1038
Db    181 AGCTGCTGGCCCGTTCG--CCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCCCCCGA 238

Qy   1039 ACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTACTGCCACCGCG 1098
Db    239 ACCCCGCCTGGA-GCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCCACTGCCACCGCG 297

Qy   1099 AAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGCCTTTC 1157
Db    298 AAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCA-CCGTTTC 356

Qy   1158 AGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGCTGTGG 1217
Db    357 AGGCCGCAGGAAGAGGAACGGAGCGAGTCCC--GCCGCGGCGCGATTCCCTGAGCTGTGG 414

Qy   1218 GACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGGGAACG 1277
Db    415 GACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGGGAACG 474

Qy   1278 CCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAAACCTG 1337
Db    475 CCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAAACCTG 534

Qy   1338 ACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAGTCGGC 1397
Db    535 ACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAGTCGGC 594

Qy   1398 CAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCTCCCGT 1457
Db    595 CAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCTCCCGT 654

Qy   1458 CTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCAGATTT 1517
Db    655 CTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCAGATTT 714

Qy   1518 TGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCCTCAACGGGGTGTGGG 1577
Db    715 TGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCTCAACGGGGTGTGGGG 774

Qy   1578 AGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAGAAGAT 1637
Db    775 AGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAGAAGAT 834

Qy   1638 CTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGGTTAGA 1697
Db    835 CTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGGTTAGA 894

Qy   1698 AGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAACCCCC 1757
Db    895 AGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAACCCCC 954

Qy   1758 ACAAGCTT 1765
Db    955 ACAAGCTT 962
```

Search completed: December 19, 2002, 14:53:39
Job time : 312 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 ; Search time 3240 Seconds
(without alignments)
15853.843 Million cell updates/sec

Title: US-09-601-267-1
Perfect score: 1765
Sequence: 1 agctactcaggaggctgaga.....gatataacccccacaagctt 1765

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1765	100.0	1765	6	AX019547	AX019547 Sequence
2	1765	100.0	1765	9	AF047386	AF047386 Homo sapi
c 3	1744.4	98.8	145829	2	AC078802	AC078802 Homo sapi
4	1719.6	97.4	2426	6	AR016035	AR016035 Sequence
5	1719.6	97.4	2426	6	AR059196	AR059196 Sequence
6	1719.6	97.4	2426	6	AR075507	AR075507 Sequence
7	1719.6	97.4	2426	6	AR081664	AR081664 Sequence
8	1719.6	97.4	2426	6	AR161905	AR161905 Sequence
9	1661.2	94.1	2420	6	I31750	I31750 Sequence 3
10	967.4	54.8	981	6	AR081665	AR081665 Sequence
11	966.4	54.8	981	6	AR028774	AR028774 Sequence
12	966.4	54.8	981	6	AX022166	AX022166 Sequence
13	965.8	54.7	981	6	A84591	A84591 Sequence 1
14	965.8	54.7	981	6	AR063825	AR063825 Sequence
15	965.8	54.7	981	6	AR079888	AR079888 Sequence
16	883.4	50.1	4118	6	A93963	A93963 Sequence 17
17	881.6	49.9	962	6	A93962	A93962 Sequence 16
18	867	49.1	867	6	AX019582	AX019582 Sequence
19	841.6	47.7	975	6	A93966	A93966 Sequence 20
20	835.4	47.3	4118	6	A93964	A93964 Sequence 18
21	835.2	47.3	975	6	A93967	A93967 Sequence 21
22	830.4	47.0	975	6	A93965	A93965 Sequence 19
23	582.8	33.0	598	9	HSU85256	U85256 Human telom
24	546.4	31.0	560	6	AR016033	AR016033 Sequence
25	546.4	31.0	560	6	AR059194	AR059194 Sequence
26	546.4	31.0	560	6	AR075505	AR075505 Sequence
27	546.4	31.0	560	6	AR161903	AR161903 Sequence
28	534.4	30.3	548	9	AF221907	AF221907 Homo sapi
29	531.4	30.1	545	9	HSU86046	U86046 Human telom
30	526.4	29.8	540	6	AR004984	AR004984 Sequence
31	523.2	29.6	540	6	AR004985	AR004985 Sequence
32	523.2	29.6	540	6	AR004986	AR004986 Sequence
33	509.2	28.8	538	6	AR004987	AR004987 Sequence
34	488	27.6	554	6	I31748	I31748 Sequence 1
35	437.4	24.8	451	6	AR183728	AR183728 Sequence
36	424	24.0	490	6	AX033369	AX033369 Sequence
37	364	20.6	541	4	AF221931	AF221931 Mustela p
38	354.2	20.1	542	4	AF221917	AF221917 Procyon l
39	350.8	19.9	540	4	AF221925	AF221925 Equus cab
40	340	19.3	541	4	AF221920	AF221920 Sus scrof
41	332	18.8	544	4	AF221939	AF221939 Felis cat
42	324.4	18.4	545	4	AF221906	AF221906 Dasypus n
43	317.6	18.0	547	4	AF221918	AF221918 Oryctolag
44	313.4	17.8	540	4	AF221936	AF221936 Bos tauru
45	276.6	15.7	830	4	AF221941	AF221941 Bos tauru

ALIGNMENTS

Applicant's not PA

RESULT 1
AX019547
LOCUS AX019547 1765 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from Patent WO9938964.
ACCESSION AX019547
VERSION AX019547.1 GI:10043461
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1765)
AUTHORS Keith,W.N.
TITLE Promoter regions of the mouse and human telomerase rna component
genes

```
  JOURNAL   Patent: WO 9938964-A 1 05-AUG-1999;
            KEITH WILLIAM NICOL (GB); CANCER RES CAMPAIGN TECH (GB)
FEATURES             Location/Qualifiers
     source          1. .1765
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      404 a    458 c    480 g    423 t
ORIGIN

  Query Match           100.0%;  Score 1765;  DB 6;  Length 1765;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1765;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420

Qy     421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960

Qy     961 GAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 GAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080

Qy    1081 GCACCTACTGCCACCGCGAAGAGTTGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGG 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GCACCTACTGCCACCGCGAAGAGTTGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGG 1140

Qy    1141 CGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGC 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGC 1200

Qy    1201 GATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCC 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCC 1260

Qy    1261 TGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTT 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTT 1320

Qy    1321 GTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAG 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAG 1380

Qy    1381 GCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCC 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCC 1440

Qy    1441 TGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGT 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGT 1500

Qy    1501 TCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCC 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCC 1560

Qy    1561 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGA 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGA 1620

Qy    1621 ATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 ATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGT 1680

Qy    1681 TTATGCCAGAGGTTAGAAGTTTCTTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGC 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TTATGCCAGAGGTTAGAAGTTTCTTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGC 1740

Qy    1741 AGTAGGATATAACCCCCACAAGCTT 1765
           |||||||||||||||||||||||||
Db    1741 AGTAGGATATAACCCCCACAAGCTT 1765


RESULT 2
AF047386
LOCUS       AF047386               1765 bp    DNA     linear   PRI 02-APR-1998
DEFINITION  Homo sapiens telomerase RNA (TR) gene, promoter and complete
            sequence.
ACCESSION   AF047386
VERSION     AF047386.1  GI:3005555
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE   1  (bases 1 to 1765)
  AUTHORS   Zhao,J.Q., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
            Black,D.M. and Keith,W.N.
  TITLE     Cloning and characterization of human and mouse telomerase RNA gene
            promoter sequences
  JOURNAL   Oncogene 16 (10), 1345-1350 (1998)
  MEDLINE   98206512
   PUBMED   9546436
REFERENCE   2  (bases 1 to 1765)
  AUTHORS   Zhao,J.Q., Hoare,S.F., McFarlane,R., Muir,S., Parkinson,E.K.,
            Black,D.M. and Keith,W.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-FEB-1998) Medical Oncology, Beatson Institute,
            Switchback Rd, Glasgow G61 1BD, UK
FEATURES             Location/Qualifiers
     source          1. .1765
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /map="3q26.3"
     gene            1. .1248
                     /gene="TR"
     promoter        1. .798
                     /gene="TR"
     misc_RNA        799. .1248
                     /gene="TR"
                     /product="telomerase RNA"
BASE COUNT      404 a    458 c    480 g    423 t
ORIGIN

  Query Match             100.0%;  Score 1765;  DB 9;  Length 1765;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1765;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420

Qy     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960

Qy     961 GAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 GAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080

Qy    1081 GCACCTACTGCCACCGCGAAGAGTTGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGG 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 GCACCTACTGCCACCGCGAAGAGTTGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGG 1140

Qy    1141 CGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 CGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGC 1200

Qy    1201 GATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCC 1260

Qy    1261 TGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTT 1320

Qy    1321 GTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 GTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAG 1380

Qy    1381 GCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCC 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 GCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCC 1440

Qy    1441 TGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 TGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGT 1500

Qy    1501 TCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCC 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCC 1560

Qy    1561 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGA 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGA 1620

Qy    1621 ATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 ATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGT 1680
```

```
Qy    1681 TTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGC 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 TTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGC 1740

Qy    1741 AGTAGGATATAACCCCCACAAGCTT 1765
           |||||||||||||||||||||||||
Db    1741 AGTAGGATATAACCCCCACAAGCTT 1765


RESULT 3
AC078802/c
LOCUS       AC078802              145829 bp    DNA     linear   HTG 19-JUN-2002
DEFINITION  Homo sapiens chromosome 3 clone RP11-816J6, WORKING DRAFT SEQUENCE,
            2 unordered pieces.
ACCESSION   AC078802
VERSION     AC078802.11  GI:21397225
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 145829)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
            Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
            Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
            Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
            Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
            Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
            Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
            Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
            Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
            Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
            Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
            Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
            Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
            Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
            Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
            Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
            Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
            Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
            Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
            Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
            Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
            Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
            Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
            Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
            Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
            Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
            Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
            Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
            Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
            Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
            Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
            Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
            Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
            Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
            Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
            Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 145829)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2000) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 145829)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUN-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Jun 13, 2002 this sequence version replaced gi:20514648.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Drafting Center Code: BCM
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: HBTL
                Center clone name: RP11-816J6
            -------------- Summary Statistics
                Sequencing vector: M13;
                Chemistry: Dye-primer Bodipy: 35% of reads
                Chemistry: Dye-terminator Big Dye: 65% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 145499 bases at least Q40
                Consensus quality: 145597 bases at least Q30
                Consensus quality: 145599 bases at least Q20
                Estimated insert size: 148612; sum-of-contigs estimation
                Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     8300: contig of 8300 bp in length
            *    8301     8400: gap of unknown length
            *    8401   145829: contig of 137429 bp in length.
FEATURES                Location/Qualifiers
     source             1. .145829
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="3"
                        /clone="RP11-816J6"
BASE COUNT    44430 a  30284 c  28482 g  42533 t    100 others
ORIGIN

  Query Match             98.8%;  Score 1744.4;  DB 2;  Length 145829;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 1759;  Conservative    0;  Mismatches    6;  Indels    1;  Gaps    1;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143993 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 143934

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143933 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 143874

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143873 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 143814

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143813 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 143754

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143753 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 143694

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
           |||||| ||||||||||||||||||||| || |||||||||| ||||||||||||||||
Db  143693 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 143634
```

```
Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143633 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 143574

Qy     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143573 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 143514

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143513 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 143454

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143453 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 143394

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143393 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 143334

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143333 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 143274

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143273 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 143214

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143213 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 143154

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143153 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 143094

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143093 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 143034

Qy     961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  143033 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 142974

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142973 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 142914

Qy    1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
           ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db  142913 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 142854

Qy    1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142853 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 142794

Qy    1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142793 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 142734

Qy    1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
           |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db  142733 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAATGGGGGCT 142674

Qy    1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142673 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 142614

Qy    1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142613 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 142554
```

```
Qy    1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142553 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 142494

Qy    1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142493 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 142434

Qy    1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142433 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 142374

Qy    1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142373 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 142314

Qy    1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  142313 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 142254

Qy    1740 CAGTAGGATATAACCCCCACAAGCTT 1765
           |||||||||||||||||||||||||
Db  142253 CAGTAGGATATAACCCCCACAAGCTT 142228
```

RESULT 4
AR016035
LOCUS AR016035 2426 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5776679.
ACCESSION AR016035
VERSION AR016035.1 GI:3972312
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2426)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 3 07-JUL-1998;
FEATURES Location/Qualifiers
source 1. .2426
/organism="unknown"
BASE COUNT 620 a 575 c 650 g 581 t
ORIGIN

Query Match 97.4%; Score 1719.6; DB 6; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

```
Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
           |||||| |||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db     961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020
```

```
Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy     961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy    1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
           ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy    1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy    1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy    1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy    1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy    1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy    1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy    1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy    1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
           ||   |  |||    ||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy    1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy    1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy    1740 CAGTAGGATATAACCCCCACAAGCTT 1765
           |||||||||||||||||||||||||
Db    2401 CAGTAGGATATAACCCCCACAAGCTT 2426
```

RESULT 5
AR059196
LOCUS AR059196 2426 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5837857.
ACCESSION AR059196
VERSION AR059196.1 GI:5984773
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2426)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5837857-A 3 17-NOV-1998;
FEATURES Location/Qualifiers
source 1. .2426
/organism="unknown"
BASE COUNT 620 a 575 c 650 g 581 t
ORIGIN

Query Match 97.4%; Score 1719.6; DB 6; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

```
Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACCCCTTTCTTTCCTAATAAAAGGGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
           |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db     961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
```

```
Db   1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy    421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy    481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy    541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy    601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy    661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy    721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy    781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy    841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy    901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy    961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy   1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy   1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
          ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy   1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy   1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy   1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy   1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy   1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy   1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy   1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy   1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
          ||   |  |||    ||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy   1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy   1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy   1740 CAGTAGGATATAACCCCCACAAGCTT 1765
          |||||||||||||||||||||||||
Db   2401 CAGTAGGATATAACCCCCACAAGCTT 2426


RESULT 6
AR075507
LOCUS       AR075507               2426 bp    DNA     linear   PAT 30-AUG-2000
DEFINITION  Sequence 4 from patent US 5958680.
ACCESSION   AR075507
VERSION     AR075507.1  GI:10002257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2426)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 5958680-A 4 28-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .2426
                     /organism="unknown"
BASE COUNT      620 a    575 c    650 g    581 t
ORIGIN

  Query Match             97.4%;  Score 1719.6;  DB 6;  Length 2426;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 1750;  Conservative    0;  Mismatches   14;  Indels    2;  Gaps    2;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy    121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy    181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy    241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy    301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db    961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy    361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db   1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy    421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy    481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy    541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy    601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy    661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy    721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy    781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy    841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy    901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy    961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy   1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy   1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
          ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy   1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy   1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy   1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy   1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy   1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy   1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy   1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy   1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
          ||    |  |||    ||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy   1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy   1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy   1740 CAGTAGGATATAACCCCCACAAGCTT 1765
          |||||||||||||||||||||||||
Db   2401 CAGTAGGATATAACCCCCACAAGCTT 2426


RESULT 7
AR081664
LOCUS       AR081664               2426 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 1 from patent US 5972605.
ACCESSION   AR081664
VERSION     AR081664.1  GI:10008390
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2426)
  AUTHORS   Villeponteau,B. and Harley,C.
  TITLE     Assays for regulators of mammalian telomerase expression
  JOURNAL   Patent: US 5972605-A 1 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .2426
                     /organism="unknown"
BASE COUNT      620 a    575 c    650 g    581 t
ORIGIN

  Query Match           97.4%;  Score 1719.6;  DB 6;  Length 2426;
  Best Local Similarity  99.1%;  Pred. No. 0;
  Matches 1750;  Conservative    0;  Mismatches   14;  Indels    2;  Gaps    2;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy    121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy    181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy    241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy    301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          |||||| ||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db    961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy    361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080
```

```
Qy    421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy    481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy    541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy    601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy    661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy    721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy    781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy    841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy    901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy    961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy   1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy   1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
          ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy   1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy   1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy   1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy   1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy   1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy   1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy   1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy   1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
          ||    |  |||    ||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy   1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy   1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy   1740 CAGTAGGATATAACCCCCACAAGCTT 1765
          |||||||||||||||||||||||||
Db   2401 CAGTAGGATATAACCCCCACAAGCTT 2426
```

```
RESULT 8
AR161905
LOCUS       AR161905               2426 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 3 from patent US 6258535.
ACCESSION   AR161905
VERSION     AR161905.1  GI:16228915
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2426)
  AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
  TITLE     Mammalian telomerase
  JOURNAL   Patent: US 6258535-A 3 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .2426
                     /organism="unknown"
BASE COUNT      620 a    575 c    650 g    581 t
ORIGIN
```

Query Match 97.4%; Score 1719.6; DB 6; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

```
Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy    121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy    181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy    241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy    301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db    961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy    361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080
```

```
Qy    421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy    481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy    541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy    601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy    661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy    721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy    781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy    841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy    901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy    961 GAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy   1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy   1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
          ||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy   1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy   1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy   1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy   1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy   1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy   1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy   1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy   1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
          ||   |  |||    ||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy   1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy   1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy   1740 CAGTAGGATATAACCCCCACAAGCTT 1765
          |||||||||||||||||||||||||
Db   2401 CAGTAGGATATAACCCCCACAAGCTT 2426
```

RESULT 9
I31750
LOCUS I31750 2420 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5583016.
ACCESSION I31750
VERSION I31750.1 GI:1822541
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2420)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US-5583016-A 3 10-DEC-1996;
FEATURES Location/Qualifiers
source 1. .2420
/organism="unknown"
BASE COUNT 620 a 572 c 647 g 581 t
ORIGIN

Query Match 94.1%; Score 1661.2; DB 6; Length 2420;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1740; Conservative 0; Mismatches 18; Indels 8; Gaps 6;

```
Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy    121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy    181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy    241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy    301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db    961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy    361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy    421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
```

```
Db   1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy    481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
Db   1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy    541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
Db   1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy    601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
Db   1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy    661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
Db   1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy    721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
Db   1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy    781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
Db   1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy    841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
Db   1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy    901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
Db   1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy    961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
Db   1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCG--CCTCCCGGGGACCTGCGGCGGGT 1678

Qy   1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
Db   1679 CGCCTGCCCAGCCCCCGAACCCCGCCTGGA-GCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1737

Qy   1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
Db   1738 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1797

Qy   1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
Db   1798 GCGAGGTTCA-CCGTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCC--GCCGCGGCG 1854

Qy   1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
Db   1855 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1914

Qy   1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
Db   1915 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1974

Qy   1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
Db   1975 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2034

Qy   1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
Db   2035 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2094

Qy   1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
Db   2095 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2154

Qy   1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
Db   2155 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2214

Qy   1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
Db   2215 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2274

Qy   1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
Db   2275 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2334

Qy   1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
Db   2335 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2394

Qy   1740 CAGTAGGATATAACCCCCACAAGCTT 1765
Db   2395 CAGTAGGATATAACCCCCACAAGCTT 2420
```

```
RESULT 10
AR081665
LOCUS       AR081665                981 bp    DNA     linear   PAT 31-AUG-2000
DEFINITION  Sequence 2 from patent US 5972605.
ACCESSION   AR081665
VERSION     AR081665.1  GI:10008391
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 981)
  AUTHORS   Villeponteau,B. and Harley,C.
  TITLE     Assays for regulators of mammalian telomerase expression
  JOURNAL   Patent: US 5972605-A 2 26-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .981
                     /organism="unknown"
BASE COUNT      172 a    303 c    306 g    200 t
ORIGIN

  Query Match           54.8%;  Score 967.4;  DB 6;  Length 981;
  Best Local Similarity   99.8%;  Pred. No. 4.7e-224;
  Matches  979;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
Db       1 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
```

```
Db    421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy   1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy   1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
          |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db    541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy   1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy   1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy   1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy   1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy   1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy   1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy   1493 AACTTAGTTCCTGCTCTGCAG 1513
          |||||||||||||||||||||
Db    961 AACTTAGTTCCTGCTCTGCAG 981


RESULT 11
AR028774
LOCUS       AR028774                981 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 5 from patent US 5858777.
ACCESSION   AR028774
VERSION     AR028774.1  GI:5940747
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 981)
  AUTHORS   Villeponteau,B., Feng,J., Andrews,W.H. and Adams,R.R.
  TITLE     Methods and reagents for regulating telomere length and telomerase
            activity
  JOURNAL   Patent: US 5858777-A 5 12-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .981
                     /organism="unknown"
BASE COUNT      172 a    303 c    305 g    200 t      1 others
ORIGIN

  Query Match           54.8%;  Score 966.4;  DB 6;  Length 981;
  Best Local Similarity 99.7%;  Pred. No. 8.2e-224;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy    534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCAGAGGATAGAAAAAAGNCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy    594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy    654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy    714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy    774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy    834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy    894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy    954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy   1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy   1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
          |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db    541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy   1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy   1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy   1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy   1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy   1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy   1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy   1493 AACTTAGTTCCTGCTCTGCAG 1513
          |||||||||||||||||||||
Db    961 AACTTAGTTCCTGCTCTGCAG 981


RESULT 12
AX022166
LOCUS       AX022166                981 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 5 from Patent EP0953042.
ACCESSION   AX022166
VERSION     AX022166.1  GI:10045843
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 981)
  AUTHORS   Andrews,W.H., Villeponteau,B., Adams,R.R. and Feng,J.
  TITLE     Methods and reagents for regulating telomere length and telomerase
```

```
          activity
  JOURNAL   Patent: EP 0953042-A 5 03-NOV-1999;
            GERON CORP (US)
FEATURES             Location/Qualifiers
     source          1. .981
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     misc_RNA        267. .715
                     /product="HTR"
                     /note="HTR TRANSCRIPT SERVES AS TEMPLATE IN THE TELOMERASE
                     RIBONUCLEOPROTEIN"
BASE COUNT      172 a    303 c    305 g    200 t      1 others
ORIGIN

  Query Match           54.8%;  Score 966.4;  DB 6;  Length 981;
  Best Local Similarity  99.7%;  Pred. No. 8.2e-224;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGNCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy    1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy    1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
           |||||||||||| |||||||||||||||||| ||||||||||||||||||||||||||||
Db     541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy    1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy    1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy    1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy    1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy    1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy    1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy    1493 AACTTAGTTCCTGCTCTGCAG 1513
           |||||||||||||||||||||
Db     961 AACTTAGTTCCTGCTCTGCAG 981


RESULT 13
A84591
LOCUS       A84591                   981 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 1 from Patent WO9845450.
ACCESSION   A84591
VERSION     A84591.1  GI:6733507
KEYWORDS    .
SOURCE      unidentified.
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 981)
  AUTHORS   Atkinson,E.M. and Kealey,J.T.
  TITLE     PURIFIED TELOMERASE
  JOURNAL   Patent: WO 9845450-A 1 15-OCT-1998;
            GERON CORP (US)
FEATURES             Location/Qualifiers
     source          1. .981
                     /organism="unidentified"
                     /db_xref="taxon:32644"
     misc_RNA        266. .716
                     /product="HTR"
                     /note="RNA COMPONENT OF HUMAN TELOMERASE (HTR)"
BASE COUNT      172 a    303 c    305 g    200 t      1 others
ORIGIN

  Query Match           54.7%;  Score 965.8;  DB 6;  Length 981;
  Best Local Similarity  99.7%;  Pred. No. 1.1e-223;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy   1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy   1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
          |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||||
Db    541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy   1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy   1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy   1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy   1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy   1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy   1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy   1493 AACTTAGTTCCTGCTCTGCAG 1513
          |||||||||||||||||||||
Db    961 AACTTAGTTCCTGCTCTGCAG 981
```

RESULT 14
AR063825

LOCUS	AR063825	981 bp DNA linear	PAT 29-SEP-1999
DEFINITION	Sequence 1 from patent US 5846723.		
ACCESSION	AR063825		
VERSION	AR063825.1 GI:5993133		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
	Unclassified.		
REFERENCE	1 (bases 1 to 981)		
AUTHORS	Kim,N.Woo., Wu,F., Kealey,J.T., Pruzan,R. and Weinrich,S.L.		
TITLE	Methods for detecting the RNA component of telomerase		
JOURNAL	Patent: US 5846723-A 1 08-DEC-1998;		
FEATURES	Location/Qualifiers		
source	1. .981		
	/organism="unknown"		
BASE COUNT	172 a 303 c 305 g 200 t	1 others	
ORIGIN			

Query Match 54.7%; Score 965.8; DB 6; Length 981;
Best Local Similarity 99.7%; Pred. No. 1.1e-223;
Matches 978; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
Qy    534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy    594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy    654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db    121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy    714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy    774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy    834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy    894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy    954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy   1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy   1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
          |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||||
Db    541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy   1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy   1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy   1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy   1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy   1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy   1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy   1493 AACTTAGTTCCTGCTCTGCAG 1513
          |||||||||||||||||||||
Db    961 AACTTAGTTCCTGCTCTGCAG 981
```

RESULT 15
AR079888

LOCUS	AR079888	981 bp DNA linear	PAT 31-AUG-2000
DEFINITION	Sequence 1 from patent US 5968506.		
ACCESSION	AR079888		
VERSION	AR079888.1 GI:10006641		
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
	Unclassified.		
REFERENCE	1 (bases 1 to 981)		
AUTHORS	Weinrich,S.L., Atkinson,E.M. III, Lichtsteiner,S.P., Vasserot,A.P., Pruzan,R.A. and Kealey,J.T.		
TITLE	Purified telomerase		

```
  JOURNAL   Patent: US 5968506-A 1 19-OCT-1999;
FEATURES             Location/Qualifiers
     source          1. .981
                     /organism="unknown"
BASE COUNT      172 a    303 c    305 g    200 t      1 others
ORIGIN

  Query Match           54.7%;  Score 965.8;  DB 6;  Length 981;
  Best Local Similarity 99.7%;  Pred. No. 1.1e-223;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy    1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy    1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
           |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db     541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy    1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy    1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy    1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy    1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy    1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy    1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy    1493 AACTTAGTTCCTGCTCTGCAG 1513
           |||||||||||||||||||||
Db     961 AACTTAGTTCCTGCTCTGCAG 981


Search completed: December 19, 2002, 14:12:02
Job time : 3320 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 ; Search time 63 Seconds
(without alignments)
8591.817 Million cell updates/sec

Title: US-09-601-267-1
Perfect score: 1765
Sequence: 1 agctactcaggaggctgaga.....gatataacccccacaagctt 1765

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1719.6	97.4	2426	1	US-08-482-115B-3	Sequence 3, Appli
2	1719.6	97.4	2426	2	US-08-660-678A-3	Sequence 3, Appli
3	1719.6	97.4	2426	2	US-08-472-802C-4	Sequence 4, Appli
4	1719.6	97.4	2426	2	US-08-714-482-1	Sequence 1, Appli
5	1719.6	97.4	2426	3	US-08-998-443-3	Sequence 3, Appli
6	1719.6	97.4	2426	4	US-09-060-523-3	Sequence 3, Appli
7	1661.2	94.1	2420	1	US-08-330-123A-3	Sequence 3, Appli
8	1661.2	94.1	2420	4	US-09-580-517-3	Sequence 3, Appli
9	1640.8	93.0	2425	2	US-08-485-778-1	Sequence 1, Appli
10	1640.8	93.0	2425	3	US-08-520-550A-1	Sequence 1, Appli
11	967.4	54.8	981	2	US-08-714-482-2	Sequence 2, Appli
12	966.4	54.8	981	2	US-08-710-249-5	Sequence 5, Appli
13	966.4	54.8	981	4	US-09-220-157A-5	Sequence 5, Appli
14	965.8	54.7	981	2	US-08-770-565-1	Sequence 1, Appli
15	965.8	54.7	981	2	US-08-833-377-1	Sequence 1, Appli
16	965.8	54.7	981	3	US-08-838-545-22	Sequence 22, Appl
17	965.8	54.7	981	4	US-09-349-532-22	Sequence 22, Appl
18	910.8	51.6	965	3	US-08-520-550A-44	Sequence 44, Appl
19	881.6	49.9	962	4	US-09-018-125-1	Sequence 1, Appli
20	546.4	31.0	560	1	US-08-482-115B-1	Sequence 1, Appli
21	546.4	31.0	560	2	US-08-660-678A-1	Sequence 1, Appli
22	546.4	31.0	560	2	US-08-472-802C-2	Sequence 2, Appli
23	546.4	31.0	560	3	US-08-998-443-1	Sequence 1, Appli
24	546.4	31.0	560	4	US-09-060-523-1	Sequence 1, Appli
25	526.4	29.8	540	1	US-08-676-967-6	Sequence 6, Appli
26	526.4	29.8	540	1	US-08-676-974-6	Sequence 6, Appli
27	526.4	29.8	540	2	US-09-098-487-6	Sequence 6, Appli
28	523.2	29.6	540	1	US-08-676-967-7	Sequence 7, Appli
29	523.2	29.6	540	1	US-08-676-967-8	Sequence 8, Appli
30	523.2	29.6	540	1	US-08-676-974-7	Sequence 7, Appli
31	523.2	29.6	540	1	US-08-676-974-8	Sequence 8, Appli
32	523.2	29.6	540	2	US-09-098-487-7	Sequence 7, Appli
33	523.2	29.6	540	2	US-09-098-487-8	Sequence 8, Appli
34	509.2	28.8	538	1	US-08-676-967-9	Sequence 9, Appli
35	509.2	28.8	538	1	US-08-676-974-9	Sequence 9, Appli
36	509.2	28.8	538	2	US-09-098-487-9	Sequence 9, Appli
37	488	27.6	554	1	US-08-330-123A-1	Sequence 1, Appli
38	488	27.6	554	4	US-09-580-517-1	Sequence 1, Appli
39	474.6	26.9	559	2	US-08-485-778-2	Sequence 2, Appli
40	474.6	26.9	559	3	US-08-520-550A-2	Sequence 2, Appli
41	472.4	26.8	486	3	US-08-630-019A-31	Sequence 31, Appl
42	468	26.5	534	2	US-09-098-487-11	Sequence 11, Appl
43	437.4	24.8	451	4	US-09-645-713-1	Sequence 1, Appli
44	408.2	23.1	448	3	US-08-520-550A-45	Sequence 45, Appl
45	367	20.8	444	3	US-08-873-709-1	Sequence 1, Appli

ALIGNMENTS

```
RESULT 1
US-08-482-115B-3
; Sequence 3, Application US/08482115B
; Patent No. 5776679
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Assays for the RNA Component of Human
;    TITLE OF INVENTION:  Telomerase
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,115B
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-000830US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2426 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-482-115B-3
```

```
Query Match             97.4%;  Score 1719.6;  DB 1;  Length 2426;
Best Local Similarity   99.1%;  Pred. No. 0;
Matches 1750;  Conservative    0;  Mismatches   14;  Indels    2;  Gaps    2;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
           |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db     961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy     961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy    1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
           ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy    1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy    1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy    1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy    1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy    1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy    1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy    1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy    1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
           ||   |  |||    ||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy    1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy    1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy    1740 CAGTAGGATATAACCCCCACAAGCTT 1765
           |||||||||||||||||||||||||
Db    2401 CAGTAGGATATAACCCCCACAAGCTT 2426
```

```
RESULT 2
US-08-660-678A-3
; Sequence 3, Application US/08660678A
; Patent No. 5837857
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Andrews, William H.
;    TITLE OF INVENTION:  Mammalian Telomerase
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
```

```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/660,678A
;       FILING DATE:  05-JUN-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/330,123
;       FILING DATE:  27-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/272,102
;       FILING DATE:  07-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Storella, John R.
;       REGISTRATION NUMBER:  32,944
;       REFERENCE/DOCKET NUMBER:  015389-000811US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2426 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-660-678A-3

  Query Match             97.4%;  Score 1719.6;  DB 2;  Length 2426;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 1750;  Conservative    0;  Mismatches   14;  Indels    2;  Gaps    2;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
Db     662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
Db     721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
Db     781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
Db     841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
Db     901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
Db     961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
Db    1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
Db    1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
Db    1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
Db    1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
Db    1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
Db    1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
Db    1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
Db    1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
Db    1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
Db    1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy     961 GAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
Db    1621 GAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
Db    1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy    1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
Db    1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy    1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
Db    1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy    1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
Db    1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy    1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
Db    1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy    1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
Db    1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy    1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
Db    2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy    1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
Db    2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy    1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
Db    2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy    1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
Db    2221 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy    1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
Db    2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy    1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
```

```
Db   2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy   1740 CAGTAGGATATAACCCCCACAAGCTT 1765
          |||||||||||||||||||||||||
Db   2401 CAGTAGGATATAACCCCCACAAGCTT 2426


RESULT 3
US-08-472-802C-4
; Sequence 4, Application US/08472802C
; Patent No. 5958680
;  GENERAL INFORMATION:
;     APPLICANT:  Villeponteau, Bryant
;     APPLICANT:  Feng, Junli
;     APPLICANT:  Andrews, William H.
;     TITLE OF INVENTION:  Mammalian Telomerase
;     NUMBER OF SEQUENCES:  44
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Townsend and Townsend and Crew LLP
;       STREET:  Two Embarcadero Center, Eighth Floor
;       CITY:  San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94111-3834
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/472,802C
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/272,102
;       FILING DATE:  07-JUL-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/330,123
;       FILING DATE:  27-OCT-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith, William M.
;       REGISTRATION NUMBER:  30,223
;       REFERENCE/DOCKET NUMBER:  15389-000820
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2426 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-472-802C-4

  Query Match             97.4%;  Score 1719.6;  DB 2;  Length 2426;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 1750;  Conservative    0;  Mismatches   14;  Indels    2;  Gaps    2;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy    121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy    181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy    241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy    301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          |||||| |||||||||||||||||||||| || |||||||||| ||||||||||||||||
Db    961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy    361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy    421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy    481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy    541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy    601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy    661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy    721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy    781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy    841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy    901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy    961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy   1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy   1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
          ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db   1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy   1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy   1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy   1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980
```

```
Qy   1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy   1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy   1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy   1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy   1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
          ||    |  |||    ||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy   1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy   1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy   1740 CAGTAGGATATAACCCCCACAAGCTT 1765
          |||||||||||||||||||||||||
Db   2401 CAGTAGGATATAACCCCCACAAGCTT 2426
```

```
RESULT 4
US-08-714-482-1
; Sequence 1, Application US/08714482
; Patent No. 5972605
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Harley, Calvin
;    TITLE OF INVENTION:  Assays for Regulators of Mammalian
;    TITLE OF INVENTION:  Telomerase Expression
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/714,482
;      FILING DATE:  16-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/521,634
;      FILING DATE:  31-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/482,115
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/472,802
;      FILING DATE:  07-JUN-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-00860US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2426 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..2426
;      OTHER INFORMATION:  /note= "SauIIIA1-HindIII fragment
;      OTHER INFORMATION:  containing hTR sequences as well as
;      OTHER INFORMATION:  transcription regulatory sequences"
US-08-714-482-1

  Query Match             97.4%;  Score 1719.6;  DB 2;  Length 2426;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 1750;  Conservative    0;  Mismatches   14;  Indels    2;  Gaps    2;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy    121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy    181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy    241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy    301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db    961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy    361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy    421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy    481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy    541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy    601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy    661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
```

```
Db    1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780

Db    1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840

Db    1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900

Db    1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960

Db    1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy     961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020

Db    1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080

Db    1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy    1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139

Db    1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy    1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199

Db    1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy    1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259

Db    1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy    1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319

Db    1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy    1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379

Db    1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy    1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439

Db    2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy    1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499

Db    2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy    1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559

Db    2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy    1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619

Db    2221 CCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy    1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679

Db    2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy    1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739

Db    2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy    1740 CAGTAGGATATAACCCCCACAAGCTT 1765

Db    2401 CAGTAGGATATAACCCCCACAAGCTT 2426
```

RESULT 5
US-08-998-443-3
; Sequence 3, Application US/08998443
; Patent No. 6054575
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,443
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678
; FILING DATE: 05-JUN-1996
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2426 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-998-443-3

Query Match 97.4%; Score 1719.6; DB 3; Length 2426;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 1750; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

```
Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60

Db    662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120

Db    721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy    121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180

Db    781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy    181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240

Db    841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900
```

```
Qy    241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy    301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          |||||| |||||||||||||||||||| || |||||||||| |||||||||||||||||||
Db    961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy    361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy    421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy    481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy    541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy    601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy    661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy    721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy    781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy    841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy    901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy    961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy   1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy   1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
          ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db   1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy   1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy   1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy   1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy   1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy   1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy   1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy   1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy   1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
          ||   |  |||    ||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 CCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy   1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy   1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy   1740 CAGTAGGATATAACCCCCACAAGCTT 1765
          |||||||||||||||||||||||||
Db   2401 CAGTAGGATATAACCCCCACAAGCTT 2426
```

RESULT 6
US-09-060-523-3
; Sequence 3, Application US/09060523
; Patent No. 6258535
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,523
; FILING DATE: 14-APR-1998
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/660,678
; FILING DATE: 05-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000813US

```
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2426 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-09-060-523-3

  Query Match             97.4%;  Score 1719.6;  DB 4;  Length 2426;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 1750;  Conservative    0;  Mismatches   14;  Indels    2;  Gaps    2;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
Db     662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
Db     721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
Db     781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
Db     841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
Db     901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
Db     961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
Db    1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
Db    1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
Db    1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
Db    1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
Db    1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
Db    1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
Db    1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
Db    1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
Db    1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
Db    1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy     961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
Db    1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
Db    1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy    1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
Db    1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy    1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
Db    1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy    1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
Db    1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy    1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
Db    1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy    1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
Db    1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy    1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
Db    2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy    1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
Db    2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy    1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
Db    2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy    1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
Db    2221 CCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy    1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
Db    2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy    1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
Db    2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy    1740 CAGTAGGATATAACCCCCACAAGCTT 1765
Db    2401 CAGTAGGATATAACCCCCACAAGCTT 2426

RESULT 7
US-08-330-123A-3
; Sequence 3, Application US/08330123A
; Patent No. 5583016
;  GENERAL INFORMATION:
;    APPLICANT:  VILLEPONTEAU, Bryant
;    APPLICANT:  FENG, Junli
;    APPLICANT:  FUNK, Walter
;    APPLICANT:  ANDREWS, William H.
```

```
;    TITLE OF INVENTION:  HUMAN TELOMERASE
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/330,123A
;      FILING DATE:  27-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  15389-000810
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2420 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-330-123A-3

  Query Match             94.1%;  Score 1661.2;  DB 1;  Length 2420;
  Best Local Similarity   98.5%;  Pred. No. 0;
  Matches 1740;  Conservative    0;  Mismatches   18;  Indels    8;  Gaps    6;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db     961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy     961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCG--CCTCCCGGGGACCTGCGGCGGGT 1678

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
          |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db    1679 CGCCTGCCCAGCCCCCGAACCCCGCCTGGA-GCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1737

Qy    1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
          ||||| |||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db    1738 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1797

Qy    1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
          |||||||||| | ||||||||||||||||||||||||||||||||||    |||||||
Db    1798 GCGAGGTTCA-CCGTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCC--GCCGCGGCG 1854

Qy    1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1855 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1914

Qy    1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1915 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1974

Qy    1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1975 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2034

Qy    1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2035 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2094

Qy    1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2095 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2154

Qy    1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2155 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2214

Qy    1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
```

```
            ||   |  |||    ||||||||||||||||||||||||||||||||||||||||||||||||
Db    2215 CCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2274

Qy    1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2275 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2334

Qy    1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2335 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2394

Qy    1740 CAGTAGGATATAACCCCCACAAGCTT 1765
           |||||||||||||||||||||||||
Db    2395 CAGTAGGATATAACCCCCACAAGCTT 2420


RESULT 8
US-09-580-517-3
; Sequence 3, Application US/09580517
; Patent No. 6320039
;   GENERAL INFORMATION:
;        APPLICANT: VILLEPONTEAU, Bryant
;                   FENG, Junli
;                   FUNK, Walter
;                   ANDREWS, William H.
;        TITLE OF INVENTION: HUMAN TELOMERASE
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend Khourie and Crew
;             STREET: 379 Lytton Avenue
;             CITY: Palo Alto
;             STATE: California
;             COUNTRY: US
;             ZIP: 94301
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/580,517
;             FILING DATE: 25-May-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/330,123
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Smith, William M
;             REGISTRATION NUMBER: 30,223
;             REFERENCE/DOCKET NUMBER: 15389-000810
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 326-2400
;             TELEFAX: (415) 326-2422
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2420 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-580-517-3

  Query Match           94.1%;  Score 1661.2;  DB 4;  Length 2420;
  Best Local Similarity  98.5%;  Pred. No. 0;
  Matches 1740;  Conservative    0;  Mismatches   18;  Indels    8;  Gaps    6;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db     662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
           |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db     961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy     421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy     541 GGATAGAAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GGATAGAAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy     961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
           |||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db    1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCG--CCTCCCGGGGACCTGCGGCGGGT 1678

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
           |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    1679 CGCCTGCCCAGCCCCCGAACCCCGCCTGGA-GCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1737

Qy    1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
           |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    1738 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1797

Qy    1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
           |||||||||| | ||||||||||||||||||||||||||||||||    |||||||
Db    1798 GCGAGGTTCA-CCGTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCC--GCCGCGGCG 1854
```

```
Qy   1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1855 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1914

Qy   1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1915 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1974

Qy   1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1975 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2034

Qy   1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2035 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2094

Qy   1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2095 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2154

Qy   1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2155 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2214

Qy   1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
          ||   |  |||    ||||||||||||||||||||||||||||||||||||||||||||
Db   2215 CCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2274

Qy   1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2275 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2334

Qy   1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2335 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2394

Qy   1740 CAGTAGGATATAACCCCCACAAGCTT 1765
          |||||||||||||||||||||||||
Db   2395 CAGTAGGATATAACCCCCACAAGCTT 2420
```

```
RESULT 9
US-08-485-778-1
; Sequence 1, Application US/08485778
; Patent No. 5876979
;  GENERAL INFORMATION:
;    APPLICANT:  Andrews, William H.
;    APPLICANT:  Avilion, Ariel Athena
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Funk, Walter
;    APPLICANT:  Greider, Carol
;    APPLICANT:  Marhuenda, Maria Antonia Blasco
;    APPLICANT:  Villeponteau, Bryant
;    TITLE OF INVENTION:  RNA COMPONENT OF TELOMERASE
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/485,778
;      FILING DATE:  07-JE-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/387,524
;      FILING DATE:  13-FEB-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/330,123
;      FILING DATE:  27-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/272,102
;      FILING DATE:  07-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  CSHL94-05A4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2425 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-485-778-1

  Query Match             93.0%;  Score 1640.8;  DB 2;  Length 2425;
  Best Local Similarity   98.4%;  Pred. No. 0;
  Matches 1742;  Conservative    0;  Mismatches   17;  Indels   11;  Gaps    8;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy    121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy    181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy    241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy    301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db    961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy    361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy    421 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy    481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy    541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy    601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy    661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
```

```
Db   1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy    721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780

Db   1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy    781 CTCGCCCGGCAGCGCACCGGGTTGC----GGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 836

Db   1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 1500

Qy    837 TTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTG 896

Db   1501 TTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTG 1560

Qy    897 TTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCAT 956

Db   1561 TTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCAT 1620

Qy    957 TCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGC 1016

Db   1621 TCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCC-GGGACCTGCGGC 1679

Qy   1017 GGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCC 1076

Db   1680 GGGTCG-CTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGG-CCGGGGCTTCTCC 1737

Qy   1077 GGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGC 1135

Db   1738 GGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGC 1797

Qy   1136 GAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGC 1195

Db   1798 GAGGGCGAGGTTCA-CCGTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGT-CCCGCGCGC 1855

Qy   1196 GGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGC 1255

Db   1856 GGCGCGATTCCCTGAGCTATGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGC 1915

Qy   1256 TTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGG 1315

Db   1916 TTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGG 1975

Qy   1316 GGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACG 1375

Db   1976 GGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACG 2035

Qy   1376 TGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGGTTGCCTGGAGCC 1435

Db   2036 TGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCC 2095

Qy   1436 GTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAAC 1495

Db   2096 GTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAAC 2155

Qy   1496 TTAGTTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACC 1555

Db   2156 TTAGTTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACC 2215

Qy   1556 AGTCCCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTT 1615

Db   2216 AGTCCCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTT 2275

Qy   1616 AATGAATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCA 1675

Db   2276 AATGAATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCA 2335

Qy   1676 TCGGTTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCT 1735

Db   2336 TCGGTTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCT 2395

Qy   1736 TGAGCAGTAGGATATAACCCCCACAAGCTT 1765

Db   2396 TGAGCAGTAGGATATAACCCCCACAAGCTT 2425
```

RESULT 10
US-08-520-550A-1
; Sequence 1, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550A
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-520-550A-1

Query Match 93.0%; Score 1640.8; DB 3; Length 2425;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 1742; Conservative 0; Mismatches 17; Indels 11; Gaps 8;

```
Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60

Db    662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120

Db    721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy    121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180

Db    781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840
```

```
Qy    181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy    241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy    301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db    961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy    361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy    421 AGTTCTCCAAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 AGTTCTCCAAAAAATGTGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy    481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy    541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy    601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy    661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy    721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy    781 CTCGCCCGGCAGCGCACCGGGTTGC----GGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 836
          |||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db   1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGAGGGTGGGCCTGGGAGGGGTGGTGGCCAT 1500

Qy    837 TTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTG 896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 TTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTG 1560

Qy    897 TTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCAT 956
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 TTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCAT 1620

Qy    957 TCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGC 1016
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   1621 TCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCC-GGGACCTGCGGC 1679

Qy    1017 GGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCC 1076
           |||||| ||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    1680 GGGTCG-CTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGG-CCGGGGCTTCTCC 1737

Qy    1077 GGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGC 1135
           |||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db    1738 GGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGC 1797

Qy    1136 GAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGC 1195
           |||||||||||||  | |||||||||||||||||||||||||||||| |||||||||
Db    1798 GAGGGCGAGGTTCA-CCGTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGT-CCCGCGCGC 1855

Qy    1196 GGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGC 1255
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    1856 GGCGCGATTCCCTGAGCTATGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGC 1915

Qy    1256 TTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGG 1315
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1916 TTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGG 1975

Qy    1316 GGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACG 1375
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1976 GGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACG 2035

Qy    1376 TGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCC 1435
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2036 TGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCC 2095

Qy    1436 GTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAAC 1495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2096 GTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAAC 2155

Qy    1496 TTAGTTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACC 1555
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2156 TTAGTTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACC 2215

Qy    1556 AGTCCCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTT 1615
           ||||||   |  |||    ||||||||||||||||||||||||||||||||||||||||
Db    2216 AGTCCCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTT 2275

Qy    1616 AATGAATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCA 1675
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2276 AATGAATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCA 2335

Qy    1676 TCGGTTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCT 1735
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2336 TCGGTTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCT 2395

Qy    1736 TGAGCAGTAGGATATAACCCCCACAAGCTT 1765
           |||||||||||||||||||||||||||||
Db    2396 TGAGCAGTAGGATATAACCCCCACAAGCTT 2425
```

RESULT 11
US-08-714-482-2
; Sequence 2, Application US/08714482
; Patent No. 5972605
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Harley, Calvin
; TITLE OF INVENTION: Assays for Regulators of Mammalian
; TITLE OF INVENTION: Telomerase Expression
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,482
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/521,634
; FILING DATE: 31-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/482,115
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:

```
;       APPLICATION NUMBER:  US 08/330,123
;       FILING DATE:  27-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/272,102
;       FILING DATE:  07-JUL-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Storella, John R.
;       REGISTRATION NUMBER:  32,944
;       REFERENCE/DOCKET NUMBER:  015389-00860US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 576-0200
;       TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  981 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  1..981
;       OTHER INFORMATION:  /note= "PstI fragment containing hTR
;       OTHER INFORMATION:  sequence"
US-08-714-482-2

  Query Match             54.8%;  Score 967.4;  DB 2;  Length 981;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-271;
  Matches  979;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy    1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy    1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
           |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db     541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy    1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy    1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy    1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy    1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy    1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy    1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy    1493 AACTTAGTTCCTGCTCTGCAG 1513
           |||||||||||||||||||||
Db     961 AACTTAGTTCCTGCTCTGCAG 981


RESULT 12
US-08-710-249-5
; Sequence 5, Application US/08710249
; Patent No. 5858777
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Andrews, William H.
;    APPLICANT:  Adams, Robert R.
;    TITLE OF INVENTION:  Methods and Reagents for Regulating
;    TITLE OF INVENTION:  Telomere Length and Telomerase Activity
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/710,249
;      FILING DATE:  13-SEP-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/583,808
;      FILING DATE:  05-JAN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/003,492
;      FILING DATE:  08-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001220US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  981 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
```

```
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  267..715
;      OTHER INFORMATION:  /product= "hTR"
;      OTHER INFORMATION:  /note= "hTR transcript serves as
;      OTHER INFORMATION:  template in the telomerase
;      OTHER INFORMATION:  ribonucleoprotein"
US-08-710-249-5

  Query Match             54.8%;  Score 966.4;  DB 2;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 3.4e-271;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy    534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db      1 CTGCAGAGGATAGAAAAAAGNCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy    594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy    654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy    714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy    774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy    834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy    894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy    954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy   1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy   1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
          |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db    541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy   1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy   1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy   1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy   1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy   1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy   1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy   1493 AACTTAGTTCCTGCTCTGCAG 1513
          |||||||||||||||||||||
Db    961 AACTTAGTTCCTGCTCTGCAG 981


RESULT 13
US-09-220-157A-5
; Sequence 5, Application US/09220157A
; Patent No. 6300110
;  GENERAL INFORMATION:
;    APPLICANT:  Villeponteau, Bryant
;    APPLICANT:  Feng, Junli
;    APPLICANT:  Andrews, William H.
;    APPLICANT:  Adams, Robert R.
;    TITLE OF INVENTION:  Methods and Reagents for Regulating
;    TITLE OF INVENTION:  Telomere Length and Telomerase Activity
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/220,157A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/710,249
;      FILING DATE:  13-SEP-1996
;      APPLICATION NUMBER:  US 08/583,808
;      FILING DATE:  05-JAN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/003,492
;      FILING DATE:  08-SEP-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001220US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  981 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  misc_RNA
;      LOCATION:  267..715
;      OTHER INFORMATION:  /product= "hTR"
;      OTHER INFORMATION:  /note= "hTR transcript serves as
;      OTHER INFORMATION:  template in the telomerase
;      OTHER INFORMATION:  ribonucleoprotein"
US-09-220-157A-5

  Query Match             54.8%;  Score 966.4;  DB 4;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 3.4e-271;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;
```

```
Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGNCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy    1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy    1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
           |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||||
Db     541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy    1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy    1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy    1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy    1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy    1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy    1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy    1493 AACTTAGTTCCTGCTCTGCAG 1513
           |||||||||||||||||||||
Db     961 AACTTAGTTCCTGCTCTGCAG 981


RESULT 14
US-08-770-565-1
; Sequence 1, Application US/08770565
; Patent No. 5846723
;  GENERAL INFORMATION:
;    APPLICANT:  Kim, Nam Woo
;    APPLICANT:  Wu, Fred
;    APPLICANT:  Kealey, James T.
;    APPLICANT:  Pruzan, Ronald
;    APPLICANT:  Weinrich, Scott L.
;    TITLE OF INVENTION:  Methods for Detecting the RNA Component of
;    TITLE OF INVENTION:  Telomerase
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TOWNSEND and TOWNSEND and CREW LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/770,565
;      FILING DATE:  20-DEC-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-002300US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-576-0200
;      TELEFAX:  415-576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  981 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-770-565-1

  Query Match             54.7%;  Score 965.8;  DB 2;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 5e-271;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420
```

```
Qy     954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy    1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy    1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
           |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db     541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy    1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy    1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720

Qy    1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy    1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy    1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy    1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy    1493 AACTTAGTTCCTGCTCTGCAG 1513
           |||||||||||||||||||||
Db     961 AACTTAGTTCCTGCTCTGCAG 981


RESULT 15
US-08-833-377-1
; Sequence 1, Application US/08833377
; Patent No. 5968506
;  GENERAL INFORMATION:
;    APPLICANT:  Weinrich, Scott L.
;    APPLICANT:  Atkinson III, Edward M.
;    APPLICANT:  Lichtsteiner, Serge P.
;    APPLICANT:  Vasserot, Alain P.
;    APPLICANT:  Pruzan, Ronald A.
;    APPLICANT:  Kealey, James T.
;    TITLE OF INVENTION:  Purified Telomerase
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/833,377
;      FILING DATE:  04-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/510,736
;      FILING DATE:  04-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Storella, John R.
;      REGISTRATION NUMBER:  32,944
;      REFERENCE/DOCKET NUMBER:  015389-001110US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  981 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  -
;      LOCATION:  1..981
;      OTHER INFORMATION:  /note= "PstI fragment of the 2.4 kb
;      OTHER INFORMATION:  Sau3IIA1-HindIII fragment of clone 28-1"
US-08-833-377-1

  Query Match             54.7%;  Score 965.8;  DB 2;  Length 981;
  Best Local Similarity   99.7%;  Pred. No. 5e-271;
  Matches  978;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy     534 CTGCAGAGGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 593
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1 CTGCAGAGGATAGAAAAAAGWCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGG 60

Qy     594 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 653
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 TCGGAAGTAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATG 120

Qy     654 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 713
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGGAAATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTC 180

Qy     714 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 773
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 TCACGAGAGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTAT 240

Qy     774 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 833
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 AAGCCGACTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGC 300

Qy     834 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 893
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 CATTTTTTGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCG 360

Qy     894 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 953
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTT 420

Qy     954 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 1013
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 CATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGC 480

Qy    1014 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 1073
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 GGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTC 540

Qy    1074 TCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGG 1132
           |||||||||||| |||||||||||||||||| |||||||||||||||||||||||||||
Db     541 TCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGG 600

Qy    1133 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 1192
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCG 660

Qy    1193 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 1252
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 CGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTT 720
```

```
Qy   1253 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 1312
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CGCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGT 780

Qy   1313 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 1372
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 GGGGGCTTGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAG 840

Qy   1373 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 1432
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 ACGTGAAGGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGA 900

Qy   1433 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 1492
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCCGTTCCTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTAC 960

Qy   1493 AACTTAGTTCCTGCTCTGCAG 1513
          |||||||||||||||||||||
Db    961 AACTTAGTTCCTGCTCTGCAG 981
```

Search completed: December 19, 2002, 13:17:18
Job time : 120 secs

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 ; Search time 69 Seconds
(without alignments)
10151.501 Million cell updates/sec

Title: US-09-601-267-1
Perfect score: 1765
Sequence: 1 agctactcaggaggctgaga.....gatataacccccacaagctt 1765

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 356696 seqs, 198428768 residues

Total number of hits satisfying chosen parameters: 713392

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1719.6	97.4	2426	10	US-09-057-351-3	Sequence 3, Appli
	2	883.4	50.1	4118	10	US-09-068-821-17	Sequence 17, Appl
	3	881.6	49.9	962	10	US-09-018-125-1	Sequence 1, Appli
	4	881.6	49.9	962	10	US-09-068-821-16	Sequence 16, Appl
	5	841.6	47.7	975	10	US-09-068-821-20	Sequence 20, Appl
	6	835.4	47.3	4118	10	US-09-068-821-18	Sequence 18, Appl
	7	835.2	47.3	975	10	US-09-068-821-21	Sequence 21, Appl
	8	830.4	47.0	975	10	US-09-068-821-19	Sequence 19, Appl
	9	546.4	31.0	560	10	US-09-057-351-1	Sequence 1, Appli
c	10	101.8	5.8	180216	10	US-09-835-232-6	Sequence 6, Appli
c	11	101.2	5.7	32193	10	US-09-764-877-2623	Sequence 2623, Ap
c	12	101.2	5.7	684973	10	US-09-263-959-1	Sequence 1, Appli
c	13	99.6	5.6	302250	10	US-09-962-832-154	Sequence 154, App
c	14	99.2	5.6	9914	10	US-09-764-847-1558	Sequence 1558, Ap
c	15	99	5.6	31994	9	US-09-764-904-71	Sequence 71, Appl
c	16	99	5.6	31994	10	US-09-764-860-599	Sequence 599, App
c	17	98.6	5.6	28897	10	US-09-764-877-3897	Sequence 3897, Ap
c	18	98	5.6	289	10	US-09-764-877-2732	Sequence 2732, Ap
c	19	97.6	5.5	2756	10	US-09-764-853-898	Sequence 898, App
c	20	97.4	5.5	27148	10	US-09-764-860-1046	Sequence 1046, Ap
	21	97	5.5	10885	10	US-09-764-877-3843	Sequence 3843, Ap
	22	96.4	5.5	30625	10	US-09-927-091-5	Sequence 5, Appli
c	23	96.4	5.5	32187	10	US-09-764-847-1550	Sequence 1550, Ap
c	24	96.4	5.5	32193	10	US-09-764-847-1549	Sequence 1549, Ap
	25	96.4	5.5	145831	10	US-09-969-708-79	Sequence 79, Appl
	26	96.4	5.5	145831	10	US-09-954-456-2116	Sequence 2116, Ap
c	27	96	5.4	303	10	US-09-764-870-604	Sequence 604, App
	28	96	5.4	1115	9	US-09-981-353-126	Sequence 126, App
c	29	96	5.4	1545	10	US-09-764-877-3172	Sequence 3172, Ap
c	30	96	5.4	10378	10	US-09-764-847-1616	Sequence 1616, Ap
c	31	96	5.4	10472	10	US-09-764-847-1615	Sequence 1615, Ap
	32	96	5.4	17752	10	US-09-748-127-3	Sequence 3, Appli
c	33	96	5.4	32185	10	US-09-764-877-3171	Sequence 3171, Ap
	34	96	5.4	32193	9	US-09-764-868-1508	Sequence 1508, Ap
c	35	96	5.4	53542	10	US-09-801-574-61	Sequence 61, Appl
c	36	96	5.4	98865	10	US-09-770-689A-3	Sequence 3, Appli
	37	95.8	5.4	2240	10	US-09-814-292-1	Sequence 1, Appli
	38	95.6	5.4	423	10	US-09-867-701-7043	Sequence 7043, Ap
c	39	95.4	5.4	36159	12	US-10-135-687-3	Sequence 3, Appli
c	40	95	5.4	32169	10	US-09-764-847-1963	Sequence 1963, Ap
c	41	95	5.4	32190	10	US-09-764-887-338	Sequence 338, App
c	42	94.8	5.4	142	10	US-09-764-877-3289	Sequence 3289, Ap
c	43	94.8	5.4	4071	10	US-09-764-869-2040	Sequence 2040, Ap
c	44	94.8	5.4	32195	10	US-09-764-870-611	Sequence 611, App
c	45	94.8	5.4	32195	10	US-09-764-870-617	Sequence 617, App

ALIGNMENTS

RESULT 1
US-09-057-351-3
; Sequence 3, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200

```
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2426 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-09-057-351-3

  Query Match             97.4%;  Score 1719.6;  DB 10;  Length 2426;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 1750;  Conservative    0;  Mismatches   14;  Indels    2;  Gaps    2;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     662 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGA-GCAGAGGTTGCAGTG 720

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 780

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCTCATCAAGACA 840

Qy     181 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 CAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAAGGGAG 900

Qy     241 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 ATTCAGTCCTTAAGATTAATAATGTAGTAGTTACACTTGATTAAAGCCATCCTCTGCTCA 960

Qy     301 AGGAGAAGCTGGAGAAGGCATTCTAAGGAAAAAGGGGCAGGGTTGGAACTCGGACGCATC 360
          |||||| |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db     961 AGGAGAGGCTGGAGAAGGCATTCTAAGGAGAAGGGGGCAGGGTAGGAACTCGGACGCATC 1020

Qy     361 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 CCACTGAGCCGAGACAAGATTCTGCTGTAGTCAGTGCTGCCTGGGAATCTATTTTCACAA 1080

Qy     421 AGTTCTCCAAAAAAATGTGATGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 AGTTCTCCAAAAAAATGTGATGATGATCAAAACTAGGAATTAGTGTTCTGTGTCTTAGGCCCTA 1140

Qy     481 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 AAATCTTCCTGTGAATTCCATTTTTAAGGTAGTCGAGGTGAACCGCGTCTGGTCTGCAGA 1200

Qy     541 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GGATAGAAAAAAGGCCCTCTGATACCTCAAGTTAGTTTCACCTTTAAAGAAGGTCGGAAG 1260

Qy     601 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 TAAAGACGCAAAGCCTTTCCCGGACGTGCGGAAGGGCAACGTCCTTCCTCATGGCCGGAA 1320

Qy     661 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 ATGGAACTTTAATTTCCCGTTCCCCCCAACCAGCCCGCCCGAGAGAGTGACTCTCACGAG 1380

Qy     721 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 AGCCGCGAGAGTCAGCTTGGCCAATCCGTGCGGTCGGCGGCCGCTCCCTTTATAAGCCGA 1440

Qy     781 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 CTCGCCCGGCAGCGCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTT 1500

Qy     841 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TGTCTAACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTT 1560

Qy     901 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 TCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTA 1620

Qy     961 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 GAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGT 1680

Qy    1021 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 CGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAG 1740

Qy    1081 GCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1139
          ||||| |||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db    1741 GCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGG 1800

Qy    1140 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 GCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCG 1860

Qy    1200 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1259
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 CGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTC 1920

Qy    1260 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 CTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCT 1980

Qy    1320 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 1379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 TGTGAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAA 2040

Qy    1380 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 1439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 GGCACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTC 2100

Qy    1440 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 1499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CTGCGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAG 2160

Qy    1500 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 1559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 TTCCTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTC 2220

Qy    1560 CCCTCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 1619
          ||   |  |||    ||||||||||||||||||||||||||||||||||||||||||||
Db    2221 CCTCAACGGGGTGTGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATG 2280

Qy    1620 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 1679
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 AATATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGG 2340

Qy    1680 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 1739
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 TTTATGCCAGAGGTTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAG 2400

Qy    1740 CAGTAGGATATAACCCCCACAAGCTT 1765
          |||||||||||||||||||||||||
Db    2401 CAGTAGGATATAACCCCCACAAGCTT 2426


RESULT 2
US-09-068-821-17
; Sequence 17, Application US/09068821
; Patent No. US20020012969A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Method of quantifying tumour
;    TITLE OF INVENTION:  cells in a body fluid and a suitable test kit
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
```

```
;       STREET:  1660 Union Street
;       CITY:  San Diego
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  92101-2926
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy Disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PADAT Sequenzmodul Version 1.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/068,821
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  DE 195 42 795.5
;       FILING DATE:  16-NOV-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Seidman, Stephanie L.
;       REGISTRATION NUMBER:  33,779
;       REFERENCE/DOCKET NUMBER:  7249-1501
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (619)238-0999
;       TELEFAX:  (619)238-0062
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  4118 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  Genomic DNA
US-09-068-821-17

  Query Match           50.1%;  Score 883.4;  DB 10;  Length 4118;
  Best Local Similarity  97.6%;  Pred. No. 1.1e-222;
  Matches  950;  Conservative    0;  Mismatches   16;  Indels    7;  Gaps    5;

Qy    794 GCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAA 853
          ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     14 GCCGCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAA 73

Qy    854 CTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTT 913
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     74 CTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTT 133

Qy    914 CAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAA 973
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134 CAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAA 193

Qy    974 ATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCC 1033
          ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db    194 ATGTCAGCTGCTGGCCCGTTCG--CCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCC 251

Qy   1034 CCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTACTGCCA 1093
          |||||||||||||||| |||||||||||||||||||||||||||||| |||||||
Db    252 CCCGAACCCCGCCTGGA-GCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCCACTGCCA 310

Qy   1094 CCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGC 1152
          |||||||||||| |||||||||||||||||||||||||||||||||||||||||||  |
Db    311 CCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCA-CC 369

Qy   1153 CTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGC 1212
            ||||||||||||||||||||||||||||||||    ||||||||||||||||||||
Db    370 GTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCC--GCCGCGGCGCGATTCCCTGAGC 427

Qy   1213 TGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGG 1272
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    428 TGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGG 487

Qy   1273 GAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAA 1332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    488 GAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAA 547

Qy   1333 ACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAG 1392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    548 ACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAG 607

Qy   1393 TCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCT 1452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    608 TCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCT 667

Qy   1453 CCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCA 1512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    668 CCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCA 727

Qy   1513 GATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCCTCAACGGGGT 1572
          ||||||||||||||||||||||||||||||||||||||||||||||||    |  |||
Db    728 GATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCTCAACGGGGTG 787

Qy   1573 GTGGGAGAACAGTCATTTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAG 1632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    788 TGGGGAGAACAGTCATTTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAG 847

Qy   1633 AAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGG 1692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    848 AAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGG 907

Qy   1693 TTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAA 1752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    908 TTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAA 967

Qy   1753 CCCCCACAAGCTT 1765
          |||||||||||||
Db    968 CCCCCACAAGCTT 980


RESULT 3
US-09-018-125-1
; Sequence 1, Application US/09018125A
; Patent No. US20010007902A1
; GENERAL INFORMATION:
;  APPLICANT: Silverman, Robert H.
;  APPLICANT: Kondo, Seiji
;  APPLICANT: Cowell, John K.
;  APPLICANT: Li, Guiying
;  APPLICANT: Torrence, Paul F.
;  TITLE OF INVENTION: RNASE L ACTIVATORS AND ANTISENSE OLIGONUCLEOTIDES
;  TITLE OF INVENTION: EFFECTIVE TO TREAT TELOMERASE-EXPRESSING MALIGNANCIES
;  FILE REFERENCE: 8656-022
;  CURRENT APPLICATION NUMBER: US/09/018,125A
;  CURRENT FILING DATE: 1999-02-03
;  EARLIER APPLICATION NUMBER: 60/044,507
;  EARLIER FILING DATE: 1997-04-21
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 962
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-018-125-1

  Query Match           49.9%;  Score 881.6;  DB 10;  Length 962;
  Best Local Similarity  73.5%;  Pred. No. 1.6e-222;
  Matches  711;  Conservative  236;  Mismatches   14;  Indels    7;  Gaps    5;

Qy    799 GGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAACTGAG 858
          |||::|||||||:|||||:|||||||:||:|||||:::::|:|:|||||:|||:|||
Db      1 GGGUUGCGGAGGGUGGGCCUGGGAGGGGUGGUGGCCAUUUUUUGUCUAACCCUAACUGAG 60

Qy    859 AAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTTCAGCG 918
          |||||||:||||||||:||::::|:|||||||||||:|:::::|:|||:|||:::|||||
Db     61 AAGGGCGUAGGCGCCGUGCUUUUGCUCCCCGCGCGCUGUUUUUCUCGCUGACUUUCAGCG 120

Qy    919 GGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAAATGTC 978
          |||||||||||:|||||:|||||::||||||::||::|:|||||||||||||||||:|:|
Db    121 GGCGGAAAAGCCUCGGCCUGCCGCCUUCCACCGUUCAUUCUAGAGCAAACAAAAAAUGUC 180
```

```
Qy     979 AGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCCCCCGA 1038
Db     181 AGCUGCUGGCCCGUUCG--CCUCCCGGGGACCUGCGGCGGGUCGCCUGCCCAGCCCCCGA 238

Qy    1039 ACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTACTGCCACCGCG 1098
Db     239 ACCCCGCCUGGA-GCCGCGGUCGGCCCGGGGCUUCUCCGGAGGCACCCACUGCCACCGCG 297

Qy    1099 AAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGCCTTTC 1157
Db     298 AAGAGUUGGGCUCUGUCAGCCGCGGGUCUCUCGGGGGCGAGGGCGAGGUUCA-CCGUUUC 356

Qy    1158 AGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGCTGTGG 1217
Db     357 AGGCCGCAGGAAGAGGAACGGAGCGAGUCCC--GCCGCGGCGCGAUUCCCUGAGCUGUGG 414

Qy    1218 GACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGGGAACG 1277
Db     415 GACGUGCACCCAGGACUCGGCUCACACAUGCAGUUCGCUUUCCUGUUGGUGGGGGGAACG 474

Qy    1278 CCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAAACCTG 1337
Db     475 CCGAUCGUGCGCAUCCGUCACCCCUCGCCGGCAGUGGGGGCUUGUGAACCCCCAAACCUG 534

Qy    1338 ACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAGTCGGC 1397
Db     535 ACUGACUGGGCCAGUGUGCUGCAAAUUGGCAGGAGACGUGAAGGCACCUCCAAAGUCGGC 594

Qy    1398 CAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCTCCCGT 1457
Db     595 CAAAAUGAAUGGGCAGUGAGCCGGGGUUGCCUGGAGCCGUUCCUGCGUGGGUUCUCCCGU 654

Qy    1458 CTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCAGATTT 1517
Db     655 CUUCCGCUUUUUGUUGCCUUUUAUGGUUGUAUUACAACUUAGUUCCUGCUCUGCAGAUUU 714

Qy    1518 TGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCCTCAACGGGGTGTGGG 1577
Db     715 UGUUGAGGUUUUUGCUUCUCCCAAGGUAGAUCUCGACCAGUCCCUCAACGGGGUGUGGGG 774

Qy    1578 AGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAGAAGAT 1637
Db     775 AGAACAGUCAUUUUUUUUUGAGAGAUCAUUUAACAUUUAAUGAAUAUUUAAUUAGAAGAU 834

Qy    1638 CTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGGTTAGA 1697
Db     835 CUAAAUGAACAUUGGAAAUUGUGUUCCUUUAAUGGUCAUCGGUUUAUGCCAGAGGUUAGA 894

Qy    1698 AGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAACCCCC 1757
Db     895 AGUUUCUUUUUUGAAAAAUUAGACCUUGGCGAUGACCUUGAGCAGUAGGAUAUAACCCCC 954

Qy    1758 ACAAGCTT 1765
Db     955 ACAAGCUU 962
```

RESULT 4
US-09-068-821-16
; Sequence 16, Application US/09068821
; Patent No. US20020012969A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method of quantifying tumour
; TITLE OF INVENTION: cells in a body fluid and a suitable test kit
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PADAT Sequenzmodul Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/068,821
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 42 795.5
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 7249-1501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 962 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-09-068-821-16

Query Match 49.9%; Score 881.6; DB 10; Length 962;
Best Local Similarity 97.8%; Pred. No. 1.6e-222;
Matches 947; Conservative 0; Mismatches 14; Indels 7; Gaps 5;

```
Qy     799 GGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAACTGAG 858
Db       1 GGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAACTGAG 60

Qy     859 AAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTTCAGCG 918
Db      61 AAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTTCAGCG 120

Qy     919 GGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAAATGTC 978
Db     121 GGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAAATGTC 180

Qy     979 AGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCCCCCGA 1038
Db     181 AGCTGCTGGCCCGTTCG--CCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCCCCCGA 238

Qy    1039 ACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTACTGCCACCGCG 1098
Db     239 ACCCCGCCTGGA-GCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCCACTGCCACCGCG 297

Qy    1099 AAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGCCTTTC 1157
Db     298 AAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCA-CCGTTTC 356

Qy    1158 AGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGCTGTGG 1217
Db     357 AGGCCGCAGGAAGAGGAACGGAGCGAGTCCC--GCCGCGGCGCGATTCCCTGAGCTGTGG 414

Qy    1218 GACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGGGAACG 1277
Db     415 GACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGGGAACG 474

Qy    1278 CCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAAACCTG 1337
Db     475 CCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAAACCTG 534

Qy    1338 ACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAGTCGGC 1397
Db     535 ACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAGTCGGC 594

Qy    1398 CAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCTCCCGT 1457
```

```
Db     595 CAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCTCCCGT 654

Qy    1458 CTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCAGATTT 1517
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     655 CTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCAGATTT 714

Qy    1518 TGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCCTCAACGGGGTGTGGG 1577
           |||||||||||||||||||||||||||||||||||||||||||||    |  |||    |||
Db     715 TGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCTCAACGGGGTGTGGGG 774

Qy    1578 AGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAGAAGAT 1637
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     775 AGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAGAAGAT 834

Qy    1638 CTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGGTTAGA 1697
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     835 CTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGGTTAGA 894

Qy    1698 AGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAACCCCC 1757
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     895 AGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAACCCCC 954

Qy    1758 ACAAGCTT 1765
           ||||||||
Db     955 ACAAGCTT 962
```

RESULT 5
US-09-068-821-20
; Sequence 20, Application US/09068821
; Patent No. US20020012969A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Method of quantifying tumour
; TITLE OF INVENTION: cells in a body fluid and a suitable test kit
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PADAT Sequenzmodul Version 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/068,821
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 42 795.5
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 7249-1501
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 975 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic RNA
US-09-068-821-20

```
  Query Match             47.7%;  Score 841.6;  DB 10;  Length 975;
  Best Local Similarity   71.3%;  Pred. No. 5.3e-212;
  Matches  690;  Conservative  232;  Mismatches   39;  Indels    7;  Gaps    5;
```

```
Qy     794 GCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAA 853
           ||  |||::||||||||:|||||:|||||||:||:|||||:::::|:|:|||||:||
Db      14 GCCGCGGGUUGCGGAGGGUGGGCCUGGGAGGGGUGGUGGCCAUUUUUUGUCUAACCCUAA 73

Qy     854 CTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTT 913
           |:||||||||||:||||||||:||::::||:|||||||||||:|:::::|:|||:|||:::
Db      74 CUGAGAAGGGCGUAGGCGCCGUGCUUUUGCUCCCCGCGCGCUGUUUUUCUCGCUGACUUU 133

Qy     914 CAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAA 973
           ||||||||||||||||:|||||:||||||::||||||::|||:::|||||||||||||
Db     134 CAGCGGGCGGAAAAGCCUCGGCCUGCCGCCUUCCACCGUUCAUUCUAGAGCAAACAAAAA 193

Qy     974 ATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCC 1033
           |:|:||||:||:|||||||::||  ||:|||||||||||:||||||||:||||:|||||||
Db     194 AUGUCAGCUGCUGGCCCGUUCG--CCUCCCGGGGACCUGCGGCGGGUCGCCUGCCCAGCC 251

Qy    1034 CCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTACTGCCA 1093
           ||||||||||||||:|||  ||||||:|||||||||||::|:|||||||||||  ||:||||
Db     252 CCCGAACCCCGCCUGGA-GCCGCGGUCGGCCCGGGGCUUCUCCGGAGGCACCCACUGCCA 310

Qy    1094 CCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGC 1152
           ||||||||||:: |||:|:|:|||||||||||:|:|:|||||||||||||||||||::||  |
Db     311 CCGCGAAGAGUUGGGCUCUGUCAGCCGCGGGUCUCUCGGGGGCGAGGGCGAGGUUCA-CC 369

Qy    1153 CTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGC 1212
           :::||||||||||||||||||||||||||||:|||    |||||||||::|||:||||
Db     370 GUUUCAGGCCGCAGGAAGAGGAACGGAGCGAGUCCC--GCCGCGGCGCGAUUCCCUGAGC 427

Qy    1213 TGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGG 1272
           :|:||||||:|||||||||||||:|||||:||||||:||||::|||:::||:|::||:|||||
Db     428 UGUGGGACGUGCACCCAGGACUCGGCUCACACAUGCAGUUCGCUUUCCUGUUGGUGGGGG 487

Qy    1273 GAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAA 1332
           ||||||||:||:||||||:|||:|||||||||:||||||||||||::|:||||||||||
Db     488 GAACGCCGAUCGUGCGCAUCCGUCACCCCUCGCCGGCAGUGGGGGCUUGUGAACCCCCAA 547

Qy    1333 ACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAG 1392
           |||:|||:|||:|||||||:|:|||:||||:|||||        :    |  |  ||
Db     548 ACCUGACUGACUGGGCCAGUGUGCUGCAAAUUGGCAGAUCGAUUCCCGUCGCCAAAUCGA 607

Qy    1393 TCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCT 1452
            |||   |   |:|||:|||||||:||||||||::|||:|||||||::||:|||:|||::|:
Db     608 GCGGGUACCAUGAAUGGGCAGUGAGCCGGGGUUGCCUGGAGCCGUUCCUGCGUGGGUUCU 667

Qy    1453 CCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCA 1512
           ||||:|::|||||::::|::|||::::|:||::|:|::|:||||||::|||::||:||:|||
Db     668 CCCGUCUUCCGCUUUUUGUUGCCUUUUAUGGUUGUAUUACAACUUAGUUCCUGCUCUGCA 727

Qy    1513 GATTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCCTCAACGGGGT 1572
           ||::::|::||||::::||::|:|||||||:|||:|||||||||:|||    |  |||
Db     728 GAUUUUGUUGAGGUUUUUGCUUCUCCCAAGGUAGAUCUCGACCAGUCCCUCAACGGGGUG 787

Qy    1573 GTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAG 1632
            ||||||||||:||:::::::::||||||:||:::||||:::||||:::|||:::|||::||
Db     788 UGGGGAGAACAGUCAUUUUUUUUUGAGAGAUCAUUUAACAUUUAAUGAAUAUUUAAUUAG 847

Qy    1633 AAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGG 1692
           ||||:|:|||:|||||::|||||::|:|::||:::||:||:||:|||:::|:||||||||
Db     848 AAGAUCUAAAUGAACAUUGGAAAUUGUGUUCCUUUAAUGGUCAUCGGUUUAUGCCAGAGG 907

Qy    1693 TTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAA 1752
           ::|||||:::|::::::|||||::|||||::|||||:||||::||||||:||||:|:||
Db     908 UUAGAAGUUUCUUUUUUGAAAAAUUAGACCUUGGCGAUGACCUUGAGCAGUAGGAUAUAA 967

Qy    1753 CCCCCACA 1760
           ||||||||
Db     968 CCCCCACA 975
```

RESULT 6
US-09-068-821-18
; Sequence 18, Application US/09068821

```
; Patent No. US20020012969A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Method of quantifying tumour
;    TITLE OF INVENTION:  cells in a body fluid and a suitable test kit
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PADAT Sequenzmodul Version 1.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/068,821
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 195 42 795.5
;      FILING DATE:  16-NOV-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  7249-1501
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4118 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
US-09-068-821-18

  Query Match           47.3%;  Score 835.4;  DB 10;  Length 4118;
  Best Local Similarity  94.6%;  Pred. No. 4.7e-210;
  Matches  920;  Conservative    0;  Mismatches   46;  Indels    7;  Gaps    5;

Qy     794 GCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAA 853
           ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      14 GCCGCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAA 73

Qy     854 CTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTT 913
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      74 CTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTT 133

Qy     914 CAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAA 973
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     134 CAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAA 193

Qy     974 ATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCC 1033
           ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db     194 ATGTCAGCTGCTGGCCCGTTCG--CCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCC 251

Qy    1034 CCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTACTGCCA 1093
           |||||||||||||||| |||||||||||||||||||||||||||||| |||||||
Db     252 CCCGAACCCCGCCTGGA-GCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCCACTGCCA 310

Qy    1094 CCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGC 1152
           |||||||||||| |||||||||||||||||||||||||||||||||||||  |
Db     311 CCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCA-CC 369

Qy    1153 CTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGC 1212
           ||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db     370 GTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCC--GCCGCGGCGCGATTCCCTGAGC 427

Qy    1213 TGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGG 1272
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     428 TGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGG 487

Qy    1273 GAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAA 1332
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     488 GAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAA 547

Qy    1333 ACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAG 1392
           ||||||||||||||||||||||||||||||||||
Db     548 ACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGATCGATGACCTAAGTGGATCCGA 607

Qy    1393 TCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCT 1452
           |   |  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     608 CTTGGTACCATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCT 667

Qy    1453 CCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCA 1512
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     668 CCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCA 727

Qy    1513 GATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCCTCAACGGGGT 1572
           ||||||||||||||||||||||||||||||||||||||||||||||||    |  |||
Db     728 GATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCTCAACGGGGTG 787

Qy    1573 GTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAG 1632
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     788 TGGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAG 847

Qy    1633 AAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGG 1692
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     848 AAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGG 907

Qy    1693 TTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAA 1752
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     908 TTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAA 967

Qy    1753 CCCCCACAAGCTT 1765
           |||||||||||||
Db     968 CCCCCACAAGCTT 980


RESULT 7
US-09-068-821-21
; Sequence 21, Application US/09068821
; Patent No. US20020012969A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Method of quantifying tumour
;    TITLE OF INVENTION:  cells in a body fluid and a suitable test kit
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PADAT Sequenzmodul Version 1.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/068,821
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 195 42 795.5
;      FILING DATE:  16-NOV-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  7249-1501
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
```

```
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  975 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic RNA
US-09-068-821-21

  Query Match             47.3%;  Score 835.2;  DB 10;  Length 975;
  Best Local Similarity   71.0%;  Pred. No. 2.6e-210;
  Matches  687;  Conservative  231;  Mismatches   43;  Indels    7;  Gaps    5;

Qy     794 GCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAA 853
           ||  ||||::|||||||||:|||||:||||||||:||:|||||::::::|:|:|||||:||
Db      14 GCCGCGGGUUGCGGAGGGUGGGCCUGGGAGGGGUGGUGGCCAUUUUUUGUCUAACCCUAA 73

Qy     854 CTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTT 913
           |:||||||||||:||||||||:||::::||:|||||||||||:|:::::|:|||:|||:::
Db      74 CUGAGAAGGGCGUAGGCGCCGUGCUUUUGCUCCCCGCGCGCUGUUUUUCUCGCUGACUUU 133

Qy     914 CAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAA 973
           ||||||||||||||||:|||||:||||||::|||||||::||::|:|||||||||||||||
Db     134 CAGCGGGCGGAAAAGCCUCGGCCUGCCGCCUUCCACCGUUCAUUCUAGAGCAAACAAAAA 193

Qy     974 ATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCC 1033
           |:|:||||:||:|||||||::||  ||:|||||||||||:||||||||:||||:||||||||
Db     194 AUGUCAGCUGCUGGCCCGUUCG--CCUCCCGGGGACCUGCGGCGGGUCGCCUGCCCAGCC 251

Qy    1034 CCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTACTGCCA 1093
           |||||||||||||:||| ||||||:||||||||||||::|:|||||||||||| ||:||||
Db     252 CCCGAACCCCGCCUGGA-GCCGCGGUCGGCCCGGGGCUUCUCCGGAGGCACCCACUGCCA 310

Qy    1094 CCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGC 1152
           ||||||||||::  |||:|:|:||||||||||:|:|:||||||||||||||||||::||   |
Db     311 CCGCGAAGAGUUGGGCUCUGUCAGCCGCGGGUCUCUCGGGGGCGAGGGCGAGGUUCA-CC 369

Qy    1153 CTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGC 1212
            :::||||||||||||||||||||||||||||:|||      |||||||||::|||:||||
Db     370 GUUUCAGGCCGCAGGAAGAGGAACGGAGCGAGUCCC--GCCGCGGCGCGAUUCCCUGAGC 427

Qy    1213 TGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGG 1272
           :|:||||||:|||||||||||:||||:||||||:||||::|||::|:::||:|::||:|||||
Db     428 UGUGGGACGUGCACCCAGGACUCGGCUCACACAUGCAGUUCGCUUUCCUGUUGGUGGGGG 487

Qy    1273 GAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAA 1332
           ||||||||:||:|||||:||||:||||:|||||||:||||||||::|:|||||||||||
Db     488 GAACGCCGAUCGUGCGCAUCCGUCACCCCUCGCCGGCAGUGGGGGCUUGUGAACCCCCAA 547

Qy    1333 ACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAG 1392
           |||:|||:|||:|||||||:|:||:|||||::|||||          |        |         |
Db     548 ACCUGACUGACUGGGCCAGUGUGCUGCAAAUUGGCAGAUCGAUCGUCCAAUCGCUAUACU 607

Qy    1393 TCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCT 1452
                |    |  |:|||:||||||:|||||||||::|||:|||||||::||:|||:|||::|:
Db     608 CUCGGUACCAUGAAUGGGCAGUGAGCCGGGGUUGCCUGGAGCCGUUCCUGCGUGGGUUCU 667

Qy    1453 CCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCA 1512
           ||||:|::||||::::|::|||:::|:||::|::|:|::|||||::||::||:|:|:|||
Db     668 CCCGUCUUCCGCUUUUUGUUGCCUUUUAUGGUUGUAUUACAACUUAGUUCCUGCUCUGCA 727

Qy    1513 GATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCCTCAACGGGGT 1572
           ||::::|::||||:::::||::|:||||||||:|||:|:||||||||:|||     |     |||
Db     728 GAUUUUGUUGAGGUUUUUGCUUCUCCCAAGGUAGAUCUCGACCAGUCCCCUCAACGGGGUG 787

Qy    1573 GTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAG 1632
             |||||||||:||:::::::::||||||:|||:::||||:::||:|||:|:::||::||
Db     788 UGGGGAGAACAGUCAUUUUUUUUUGAGAGAUCAUUUAACAUUUAAUGAAUAUUUAAUUAG 847

Qy    1633 AAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGG 1692
           ||||:|:|||:|||||::|||||::|:|::||:::||:||:||:|||:::|:||||||||
Db     848 AAGAUCUAAAUGAACAUUGGAAAUUGUGUUCCUUUAAUGGUCAUCGGUUUAUGCCAGAGG 907

Qy    1693 TTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAA 1752
           ::|||||:::|:::::::|||||||::||||::||||||:|||||::||||||:||||:|:||
Db     908 UUAGAAGUUUCUUUUUUGAAAAAUUAGACCUUGGCGAUGACCUUGAGCAGUAGGAUAUAA 967

Qy    1753 CCCCCACA 1760
           ||||||||
Db     968 CCCCCACA 975


RESULT 8
US-09-068-821-19
; Sequence 19, Application US/09068821
; Patent No. US20020012969A1
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Method of quantifying tumour
;    TITLE OF INVENTION:  cells in a body fluid and a suitable test kit
;    NUMBER OF SEQUENCES:  21
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PADAT Sequenzmodul Version 1.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/068,821
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE 195 42 795.5
;      FILING DATE:  16-NOV-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L.
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  7249-1501
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)238-0999
;      TELEFAX:  (619)238-0062
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  975 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic RNA
US-09-068-821-19

  Query Match             47.0%;  Score 830.4;  DB 10;  Length 975;
  Best Local Similarity   70.7%;  Pred. No. 4.7e-209;
  Matches  684;  Conservative  231;  Mismatches   46;  Indels    7;  Gaps    5;

Qy     794 GCACCGGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAA 853
           ||  ||||::|||||||||:|||||:||||||||:||:|||||::::::|:|:|||||:||
Db      14 GCCGCGGGUUGCGGAGGGUGGGCCUGGGAGGGGUGGUGGCCAUUUUUUGUCUAACCCUAA 73

Qy     854 CTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTT 913
           |:||||||||||:||||||||:||::::||:|||||||||||:|:::::|:|||:|||:::
Db      74 CUGAGAAGGGCGUAGGCGCCGUGCUUUUGCUCCCCGCGCGCUGUUUUUCUCGCUGACUUU 133

Qy     914 CAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAA 973
           ||||||||||||||||:|||||:||||||::|||||||::||::|:|||||||||||||||
Db     134 CAGCGGGCGGAAAAGCCUCGGCCUGCCGCCUUCCACCGUUCAUUCUAGAGCAAACAAAAA 193

Qy     974 ATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCC 1033
           |:|:||||:||:|||||||::||  ||:|||||||||||:||||||||:||||:||||||||
Db     194 AUGUCAGCUGCUGGCCCGUUCG--CCUCCCGGGGACCUGCGGCGGGUCGCCUGCCCAGCC 251
```

```
Qy   1034 CCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTACTGCCA 1093
          |||||||||||||:||| |||||||:|||||||||||::|:||||||||||| ||:||||
Db    252 CCCGAACCCCGCCUGGA-GCCGCGGUCGGCCCGGGGCUUCUCCGGAGGCACCCACUGCCA 310

Qy   1094 CCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGC 1152
          ||||||||||:: |||:|:|:||||||||||:|:|:|||||||||||||||||::||  |
Db    311 CCGCGAAGAGUUGGGCUCUGUCAGCCGCGGGUCUCUCGGGGGCGAGGGCGAGGUUCA-CC 369

Qy   1153 CTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGC 1212
           :::||||||||||||||||||||||||||||:|||    ||||||||||::|||:||||
Db    370 GUUUCAGGCCGCAGGAAGAGGAACGGAGCGAGUCCC--GCCGCGGCGCGAUUCCCUGAGC 427

Qy   1213 TGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGG 1272
          :|:||||||:|||||||||||:||||:||||||:||||::|||:::||:|::||:|||||
Db    428 UGUGGGACGUGCACCCAGGACUCGGCUCACACAUGCAGUUCGCUUUCCUGUUGGUGGGGG 487

Qy   1273 GAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAA 1332
          |||||||||:||:|||||:|||:||||||:|||||||||:||||||::|:||||||||||
Db    488 GAACGCCGAUCGUGCGCAUCCGUCACCCCUCGCCGGCAGUGGGGGCUUGUGAACCCCCAA 547

Qy   1333 ACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGCACCTCCAAAG 1392
          |||:|||:|||:|||||||:|:||:|||||::|||||
Db    548 ACCUGACUGACUGGGCCAGUGUGCUGCAAAUUGGCAGAUCGAUGACCUAAGUGGAUCCGA 607

Qy   1393 TCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTGCGTGGGTTCT 1452
             |  |  |:|||:||||||:|||||||||::|||:|||||||::||:|||:|||::|:
Db    608 CUUGGUACCAUGAAUGGGCAGUGAGCCGGGGUUGCCUGGAGCCGUUCCUGCGUGGGUUCU 667

Qy   1453 CCCGTCTTCCGCTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTCCTGCTCTGCA 1512
          ||||:|::||||::::|::|||::::|:||::|:|::|||||::||::||:||:|:|||
Db    668 CCCGUCUUCCGCUUUUGUUGCCUUUUAUGGUUGUAUUACAACUUAGUUCCUGCUCUGCA 727

Qy   1513 GATTTTGTTGAGGTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCCTCAACGGGGT 1572
          ||::::|::||||::::||::|:||||||||:|||:|:|||||||||:|||      |   |||
Db    728 GAUUUUGUUGAGGUUUUGCUUCUCCCAAGGUAGAUCUCGACCAGUCCCUCAACGGGGUG 787

Qy   1573 GTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAATATTTAATTAG 1632
            ||||||||||:||:::::::::||||||:||:::||||:::||:|||:|:::||::||
Db    788 UGGGAGAACAGUCAUUUUUUUUUGAGAGAUCAUUUAACAUUUAAUGAAUAUUUAAUUAG 847

Qy   1633 AAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCATCGGTTTATGCCAGAGG 1692
          ||||:|:|||:|||||::|||||::|:|::||:::||:||:||:|||:::|:||||||||
Db    848 AAGAUCUAAAUGAACAUUGGAAAUUGUGUUCCUUUAAUGGUCAUCGGUUUAUGCCAGAGG 907

Qy   1693 TTAGAAGTTTCTTTTTTGAAAAATTAGACCTTGGCGATGACCTTGAGCAGTAGGATATAA 1752
          ::|||||:::|::::::||||||::|||||::|||||:||||::||||||:||||:|:||
Db    908 UUAGAAGUUUCUUUUUUGAAAAAUUAGACCUUGGCGAUGACCUUGAGCAGUAGGAUAUAA 967

Qy   1753 CCCCCACA 1760
          ||||||||
Db    968 CCCCCACA 975
```

RESULT 9
US-09-057-351-1
; Sequence 1, Application US/09057351
; Patent No. US20010034439A1
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/057,351
; FILING DATE: 08-APR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,802
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000821US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-09-057-351-1

```
  Query Match             31.0%;  Score 546.4;  DB 10;  Length 560;
  Best Local Similarity   80.7%;  Pred. No. 2.1e-134;
  Matches  452;  Conservative  106;  Mismatches    1;  Indels    1;  Gaps    1;

Qy    799 GGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAACTGAG 858
          |||::||||||||:|||||:||||||||:||:|||||::::::|:|:|||||:|||:|||
Db      1 GGGUUGCGGAGGGUGGGCCUGGGAGGGGUGGUGGCCAUUUUUUGUCUAACCCUAACUGAG 60

Qy    859 AAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTTCAGCG 918
          |||||||:||||||||:||::::||:||||||||||:|:::::|:|||:|||:::|||||
Db     61 AAGGGCGUAGGCGCCGUGCUUUUGCUCCCCGCGCGCUGUUUUUCUCGCUGACUUUCAGCG 120

Qy    919 GGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAAATGTC 978
          ||||||||||||:|||||:||||||::||||||::||::|:|||||||||||||||:|:|
Db    121 GGCGGAAAAGCCUCGGCCUGCCGCCUUCCACCGUUCAUUCUAGAGCAAACAAAAAAUGUC 180

Qy    979 AGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCCCCCGA 1038
          |||:||:||||||::||||||:||||||||||:||||||||:||||:|||||||||||||
Db    181 AGCUGCUGGCCCGUUCGCCCCUCCCGGGGACCUGCGGCGGGUCGCCUGCCCAGCCCCCGA 240

Qy   1039 ACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTACTGCCACCGCG 1098
          ||||||||:|||||||||||:|||||||||||::|:||||||||||| ||:|||||||||
Db    241 ACCCCGCCUGGAGGCCGCGGUCGGCCCGGGGCUUCUCCGGAGGCACCCACUGCCACCGCG 300

Qy   1099 AAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGCCTTTC 1157
          |||||:: |||:|:|:||||||||||:|:|:||||||||||||||||::||||||:::|
Db    301 AAGAGUUGGGCUCUGUCAGCCGCGGGUCUCUCGGGGGCGAGGGCGAGGUUCAGGCCUUUC 360

Qy   1158 AGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGCTGTGG 1217
          |||||||||||||||||||||||||||:|||||||||||||||||::|||:||||:|:||
Db    361 AGGCCGCAGGAAGAGGAACGGAGCGAGUCCCCGCGCGCGGCGCGAUUCCCUGAGCUGUGG 420

Qy   1218 GACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGGTGGGGGAACG 1277
          ||||:|||||||||||:||||:||||||:||||::|||:::||:|::||:|||||||||
Db    421 GACGUGCACCCAGGACUCGGCUCACACAUGCAGUUCGCUUUCCUGUUGGUGGGGGAACG 480

Qy   1278 CCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAACCCCCAAACCTG 1337
          ||||:||:|||||:|||:||||||:|||||||||:||||||::|:|||||||||||||:|
Db    481 CCGAUCGUGCGCAUCCGUCACCCCUCGCCGGCAGUGGGGGCUUGUGAACCCCCAAACCUG 540

Qy   1338 ACTGACTGGGCCAGTGTGCT 1357
```

```
          ||:|||:|||||||:|:||:
Db    541 ACUGACUGGGCCAGUGUGCU 560


RESULT 10
US-09-835-232-6/c
; Sequence 6, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
;  APPLICANT: Leder, Philip
;  APPLICANT:  Leader, Benjamin
;  TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: 00383/052002
;  CURRENT APPLICATION NUMBER: US/09/835,232
;  CURRENT FILING DATE:  2001-04-12
;  PRIOR APPLICATION NUMBER: US 60/196,811
;  PRIOR FILING DATE: 2000-04-13
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 180216
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(180216)
;   OTHER INFORMATION: n = A,T,C or G
US-09-835-232-6

  Query Match             5.8%;  Score 101.8;  DB 10;  Length 180216;
  Best Local Similarity   88.5%;  Pred. No. 4.4e-16;
  Matches  123;  Conservative    0;  Mismatches   12;  Indels    4;  Gaps    1;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||||||||||||| || |||||| |||||||||||||||| ||||||||||||
Db  64485 AGCTACTCAGGAGGCTGAGGCAGGAGAATTGCTTGAACCCGGGAGGCGGAGGTTGCAGTG 64426

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          |||||||||| |||||||| ||    |||||||||||| | ||||| ||||||||||||
Db  64425 AGCCGAGATCGCGCCACTACAC----TCCAGCCTGGGCAACAGAGCGAGACTCCGTCTCA 64370

Qy    121 AAAAAAAAAATCGTTACAA 139
          ||||||||||  |||| ||
Db  64369 AAAAAAAAAAAGTTATAA 64351


RESULT 11
US-09-764-877-2623/c
; Sequence 2623, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC005
;  CURRENT APPLICATION NUMBER: US/09/764,877
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - refer to PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 4031
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2623
;   LENGTH: 32193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-877-2623

  Query Match             5.7%;  Score 101.2;  DB 10;  Length 32193;
  Best Local Similarity   86.2%;  Pred. No. 2.7e-16;
  Matches  112;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||| |||||||||| || |||||||||||||||| |||||||||||||| || ||
Db  31984 AGCTACTCTGGAGGCTGAGGCAGGAGAATCGCTTGAACCCAGGAGGCAGAGGTTACAATG 31925

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||| |||||| |||||| |||| |||||||||||| | |||| |||||||  |||||
Db  31924 AGCTGAGATCGTGCCACTGCACTCACTCCAGCCTGGGCAACAGAGTAAGACTCTATCTCA 31865

Qy    121 AAAAAAAAAA 130
          ||||||||||
Db  31864 AAAAAAAAAA 31855


RESULT 12
US-09-263-959-1/c
; Sequence 1, Application US/09263959
; Patent No. US20020150891A1
;  GENERAL INFORMATION:
;    APPLICANT:  Hood, Leroy E.
;    APPLICANT:  Rowen, Lee
;    APPLICANT:  Koop, Ben F.
;    TITLE OF INVENTION:  DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH U
;    NUMBER OF SEQUENCES:  1279
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Seed and Berry LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  US
;      ZIP:  98104-7092
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/263,959
;      FILING DATE:  05-MAR-1999
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McMasters, David D.
;      REGISTRATION NUMBER:  33,963
;      REFERENCE/DOCKET NUMBER:  920010.426C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  684973 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-263-959-1

  Query Match             5.7%;  Score 101.2;  DB 10;  Length 684973;
  Best Local Similarity   86.2%;  Pred. No. 1.2e-15;
  Matches  112;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||| |||||||||| || |||||| || | |||||||||||||||| ||||||||
Db 442801 AGCTACTCGGGAGGCTGAGGCAGGAGAATGGCGTAAACCCGGGAGGCAGAGCTTGCAGTG 442742

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          ||||||||||  ||||||  |||||||||||||||| || ||||| | |||| ||||||
Db 442741 AGCCGAGATCGTGCCACTGCACTCCATCCAGCCTGGGAGACAGAGCGACACTCTGTCTCA 442682

Qy    121 AAAAAAAAAA 130
          ||| |||| |
Db 442681 AAAGAAAAGA 442672


RESULT 13
US-09-962-832-154/c
; Sequence 154, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Ebner, Reinhard
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-74
;  CURRENT APPLICATION NUMBER: US/09/962,832
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,077
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,280
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 154
;   LENGTH: 302250
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-962-832-154

  Query Match             5.6%;  Score 99.6;  DB 10;  Length 302250;
  Best Local Similarity   85.4%;  Pred. No. 2.2e-15;
  Matches  111;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||| |||||||||| ||  |||||||||||||||||||||| |||| ||| |||
Db 226482 AGCTACTCGGGAGGCTGAGGCAGAAGAATCGCTTGAACCCGGGAGGCGGAGGCTGCGGTG 226423

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          |||||||||||| |||||  |||| |   |||||||||| ||||| ||||||| |||||
Db 226422 AGCCGAGATCACACCACTGTACTCGACAGAGCCTGGGCGACAGAGCGAGACTCCATCTCA 226363

Qy    121 AAAAAAAAAA 130
          |||| ||| |
Db 226362 AAAACAAACA 226353


RESULT 14
US-09-764-847-1558/c
; Sequence 1558, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC009
;  CURRENT APPLICATION NUMBER: US/09/764,847
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 2003
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1558
;   LENGTH: 9914
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-847-1558

  Query Match             5.6%;  Score 99.2;  DB 10;  Length 9914;
  Best Local Similarity   78.2%;  Pred. No. 5e-16;
  Matches  133;  Conservative    0;  Mismatches   33;  Indels    4;  Gaps    1;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          |||||||||| |||||||| || ||||||||||||||| ||||||||||||||||||||
Db   8437 AGCTACTCAGAAGGCTGAGGCAGGAGAATCGCTTGAACCTGGGAGGCAGAGGTTGCAGTG 8378

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          |||| ||||   ||||||  ||||    ||||||||| || ||||||||||| ||||||
Db   8377 AGCCAAGATTGTGCCACTGCACTC----CAGCCTGGGTGACAGAGCAAGACTCTGTCTCA 8322

Qy    121 AAAAAAAAAATCGTTACAATTTATGGTGGATTACTCCCCTCTTTTTACCT 170
          |||||||||| |||    ||| |  |  |||| |   |||  |  | |
Db   8321 AAAAAAAAAATTGTTTTTTTTTTTTTTTAATTAGCCAGGTCTGGTGGCAT 8272


RESULT 15
US-09-764-904-71/c
; Sequence 71, Application US/09764904
; Patent No. US20020173454A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PA122
;  CURRENT APPLICATION NUMBER: US/09/764,904
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 137
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 71
;   LENGTH: 31994
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-904-71

  Query Match             5.6%;  Score 99;  DB 9;  Length 31994;
  Best Local Similarity   82.0%;  Pred. No. 1e-15;
  Matches  114;  Conservative    0;  Mismatches   25;  Indels    0;  Gaps    0;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
          || ||||  |||||||||||||| |||||||||||||| |||||||  ||||||||||||
Db   5801 AGTTACTTGGGAGGCTGAGACAGGAGAATCGCTTGAACTCGGGAGGTGGAGGTTGCAGTG 5742

Qy     61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
          |||||||||  | ||| |  || ||| |||||||||||| | ||||||||||  ||||||
Db   5741 AGCCGAGATGGCACCATTGCACCCCAGCCAGCCTGGGCAACAGAGCAAGACTATGTCTCA 5682

Qy    121 AAAAAAAAAATCGTTACAA 139
          |||| |||||     ||||
Db   5681 AAAACAAAAACAAAAACAA 5663


Search completed: December 19, 2002, 15:13:48
Job time : 1612 secs
```

GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 19, 2002, 12:14:29 ; Search time 2130 Seconds
(without alignments)
13420.204 Million cell updates/sec

Title: US-09-601-267-1
Perfect score: 1765
Sequence: 1 agctactcaggaggctgaga.....gatataacccccacaagctt 1765

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	424.2	24.0	443	9	AI825849	AI825849 td19d01.x
c	2	390.8	22.1	421	10	AW293800	AW293800 UI-H-BI2-
c	3	371.4	21.0	412	10	AW136367	AW136367 UI-H-BI1-
c	4	355.4	20.1	376	9	AI380754	AI380754 tf97g05.x
c	5	355.2	20.1	388	10	AW207347	AW207347 UI-H-BI1-
c	6	351.4	19.9	353	14	BM695101	BM695101 UI-E-CL1-
c	7	110.8	6.3	466	17	AQ229478	AQ229478 HS_2021_A
	8	109.2	6.2	680	17	AG186502	AG186502 Pan trogl
	9	107.6	6.1	418	17	AQ390169	AQ390169 CITBI-E1-
	10	107.2	6.1	469	13	BM509394	BM509394 ih17f10.y
	11	107.2	6.1	516	13	BI468297	BI468297 id87b01.y
	12	107.2	6.1	529	14	BQ270800	BQ270800 ik05b06.y
	13	107.2	6.1	556	14	BQ267333	BQ267333 ik02c03.y
	14	107.2	6.1	589	14	BQ270346	BQ270346 ik09g10.y
	15	106.4	6.0	635	17	AQ428429	AQ428429 CITBI-E1-
	16	106	6.0	774	17	AQ751486	AQ751486 HS_5576_B
	17	104.8	5.9	671	17	AQ418931	AQ418931 RPCI-11-1
	18	104.6	5.9	465	17	AQ527107	AQ527107 CITBI-E1-
	19	104.6	5.9	815	14	BQ429052	BQ429052 AGENCOURT
c	20	104.4	5.9	303	14	BM672404	BM672404 UI-E-CQ0-
c	21	104.4	5.9	712	17	AG139751	AG139751 Pan trogl
	22	103.8	5.9	451	14	N66929	N66929 za47h09.s1
c	23	103	5.8	837	13	BI820230	BI820230 603037070
	24	103	5.8	1074	14	BQ429712	BQ429712 AGENCOURT
c	25	102.8	5.8	318	13	BI492686	BI492686 df27g08.w
	26	102.8	5.8	340	10	AW021747	AW021747 df27g08.y
c	27	102.8	5.8	684	17	AG109444	AG109444 Pan trogl
c	28	102	5.8	364	17	AQ333390	AQ333390 HS_5010_A
c	29	101.6	5.8	256	9	AA084337	AA084337 zn04b05.s
	30	101.2	5.7	382	10	AV764523	AV764523 AV764523
c	31	101.2	5.7	474	9	AI866580	AI866580 tz51c10.x
c	32	101.2	5.7	514	17	B37536	B37536 HS-1044-A1-
c	33	101.2	5.7	735	9	AU120382	AU120382 AU120382
	34	101.2	5.7	773	12	BG221771	BG221771 RST41586
	35	101.2	5.7	815	12	BF382750	BF382750 601816513
c	36	101.2	5.7	859	17	AQ750588	AQ750588 HS_5573_B
	37	101.2	5.7	925	12	BG249993	BG249993 602362061
	38	101	5.7	445	17	AQ198078	AQ198078 RPCI11-46
	39	100.4	5.7	504	9	AL138096	AL138096 DKFZp547B
c	40	100.2	5.7	335	9	AA492202	AA492202 ng78e08.s
c	41	100	5.7	459	17	AQ483064	AQ483064 RPCI-11-2
	42	99.8	5.7	404	14	W07861	W07861 zb04g03.r1
c	43	99.8	5.7	460	9	AI597733	AI597733 tu91a08.x
c	44	99.8	5.7	464	10	AW150226	AW150226 xg49d01.x
c	45	99.8	5.7	662	17	AQ262070	AQ262070 CITBI-E1-

ALIGNMENTS

RESULT 1
AI825849/c
LOCUS AI825849 443 bp mRNA linear EST 24-AUG-1999
DEFINITION td19d01.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2076097 3', mRNA sequence.
ACCESSION AI825849
VERSION AI825849.1 GI:5446520
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 443)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
FEATURES Location/Qualifiers

```
    source          1. .443
                    /organism="Homo sapiens"
                    /db_xref="taxon:9606"
                    /clone="IMAGE:2076097"
                    /clone_lib="NCI_CGAP_Co16"
                    /tissue_type="colon tumor, RER+"
                    /lab_host="DH10B"
                    /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                    modified polylinker; Site_1: Not I; Site_2: Eco RI;
                    Plasmid DNA from the normalized library NCI_CGAP_Co10 was
                    prepared, and ss circles were made in vitro. Following HAP
                    purification, this DNA was used as tracer in a subtractive
                    hybridization reaction. The driver was PCR-amplified cDNAs
                    from a pool of 5,000 clones made from the same library
                    (cloneIDs 1057416-1061255, and 1144584-1145351).
                    Subtraction by Bento Soares and M. Fatima Bonaldo.  "
BASE COUNT       78 a    144 c    151 g     68 t      2 others
ORIGIN

  Query Match             24.0%;  Score 424.2;  DB 9;  Length 443;
  Best Local Similarity   98.6%;  Pred. No. 1.7e-94;
  Matches  437;  Conservative    0;  Mismatches    5;  Indels    1;  Gaps    1;

Qy     895 TGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTC 954
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     443 TGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTC 384

Qy     955 ATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCG 1014
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     383 ATTCTAGAGCAAACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCG 324

Qy    1015 GCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCT 1074
           |||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||
Db     323 GCGGGTCGCCTGCCCAGCCNCCGAACNCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCT 264

Qy    1075 CCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGG 1133
           |||||||||| |||||||||||||||||| ||||||||||||||||||||||||||||||
Db     263 CCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGG 204

Qy    1134 GCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGC 1193
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     203 GCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGC 144

Qy    1194 GCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTC 1253
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     143 GCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTC 84

Qy    1254 GCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTG 1313
           |||||||||||||||||||||||||||||| |||||||||||||||||||||||| ||
Db      83 GCTTTCCTGTTGGTGGGGGGAACGCCGATCGTGAGCATCCGTCACCCCTCGCCGGCAATG 24

Qy    1314 GGGGCTTGTGAACCCCCAAACCT 1336
           |||||||||||||||||||||||
Db      23 GGGGCTTGTGAACCCCCAAACCT 1


RESULT 2
AW293800/c
LOCUS       AW293800                421 bp    mRNA    linear   EST 16-JAN-2000
DEFINITION  UI-H-BI2-ahp-f-04-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone
            IMAGE:2727679 3', mRNA sequence.
ACCESSION   AW293800
VERSION     AW293800.1  GI:6700436
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 421)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            NCI-CGAP clone distribution information can be found through the
            I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html The following repetitive
            elements were found in this cDNA sequence: 197-273,
            >GC_rich#Low_complexity
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES                Location/Qualifiers
     source             1. .421
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /clone="IMAGE:2727679"
                        /clone_lib="NCI_CGAP_Sub4"
                        /lab_host="DH10B (Life Technologies)"
                        /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                        polylinker; Site_1: Not I; Site_2: Eco RI; The
                        NCI_CGAP_Sub4 library is a subtracted library derived from
                        the  NCI_CGAP_Sub2 library which is a subtracted library
                        derived from  the NCI_CGAP_Sub1 library, which is a
                        subtracted library derived  from BI. BI constitutes a
                        mixture of 21 normalized or subtracted  NCI_CGAP
                        libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28,
                        NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5,
                        NCI_CGAP_Kid12,  NCI_CGAP_Kid3, NCI_CGAP_Kid11,
                        NCI_CGAP_Lym2, NCI_CGAP_Br2,  NCI_CGAP_Co8, NCI_CGAP_CLL1,
                        NCI_CGAP_Lei2, NCI_CGAP_Brn23,  NCI_CGAP_Lu5,
                        NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
                        NCI_CGAP_Brn25. These 21 libraries were pooled and a
                        single-stranded DNA  preparation of the resulting mixture
                        was used as a tracer in a subtractive  hybridization with
                        a driver whose composition is detailed below:
                        NCI_CGAP_Kid3 pool 1 : LLAM 3334-3337, 3682-3683,
                        3798-3803  (IMAGE CloneIDs 1322376-1323911,
                        1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 :
                        LLAM 3338-3342, 3722-3725, 3776-3778  (IMAGE CloneIDs
                        1323912-1325831, 1471368-1472903, 1492104-1493255)
                        NCI_CGAP_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE
                        CloneIDs 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4
                        pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
                        CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743
                        ) NCI_CGAP_Pr22 pool 1 : LLAM 2457-2459, 2758-2759,
                        3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959,
                        1217928-1220615) NCI_CGAP_Co10 pool 1 : LLAM 2644-2653,
                        2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351
                        ) Subtraction was performed as previously described
                        [Bonaldo, Lennon & Soares (1996): Normalization and
                        Subtraction:  Two Approaches To Facilitate Gene Discovery.
                        Genome Research 6, 791-806.]
                        TAG_LIB=NCI_CGAP_Co10
                        TAG_TISSUE=colon
                        TAG_SEQ=AAACG"
BASE COUNT       68 a    135 c    143 g     75 t
ORIGIN

  Query Match             22.1%;  Score 390.8;  DB 10;  Length 421;
  Best Local Similarity   99.3%;  Pred. No. 3.2e-86;
  Matches  403;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy     846 AACCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCG 905
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 ACCCCTAACTGAGAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCG 362

Qy     906 CTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCA 965
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCA 302

Qy     966 AACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCT 1025
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 AACAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCT 242

Qy    1026 GCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACC 1085
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 GCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACC 182

Qy    1086 TACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAG 1144
          |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db     181 CACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAG 122

Qy    1145 GTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATT 1204
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATT 62

Qy    1205 CCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAG 1250
          ||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAG 16


RESULT 3
AW136367/c
LOCUS       AW136367                412 bp    mRNA    linear   EST 29-OCT-1999
DEFINITION  UI-H-BI1-acn-h-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
            IMAGE:2715099 3', mRNA sequence.
ACCESSION   AW136367
VERSION     AW136367.1  GI:6140500
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 412)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            NCI-CGAP clone distribution information can be found through the
            I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html The following repetitive
            elements were found in this cDNA sequence: 200-276,
            >GC_rich#Low_complexity
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .412
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2715099"
                      /clone_lib="NCI_CGAP_Sub3"
                      /lab_host="DH10B (Life Technologies)"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; The
                      NCI_CGAP_Sub3 library is a subtracted library derived from
                      the  NCI_CGAP_Sub1 library, which is a subtracted library
                      derived from BI.  BI constitutes a mixture of 21
                      normalized or subtracted NCI_CGAP  libraries: NCI_CGAP_Co4
                      , NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
                      NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
                      NCI_CGAP_Kid3,  NCI_CGAP_Kid11, NCI_CGAP_Lym2,
                      NCI_CGAP_Br2, NCI_CGAP_Co8,  NCI_CGAP_CLL1, NCI_CGAP_Lei2,
                      NCI_CGAP_Brn23, NCI_CGAP_Lu5,  NCI_CGAP_Lu24,
                      NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
                      NCI_CGAP_Brn25.  These 21 libraries were pooled and a
                      single-stranded DNA  preparation of the resulting mixture
                      was used as a tracer in a subtractive  hybridization with
                      a driver whose composition is detailed below:
                      NCI_CGAP_Kid3 pool 1    LLAM 3334-3337, 3682-3683,
                      3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775
                      , 1500552-1502855); NCI_CGAP_Kid5 pool 1    LLAM 3338-3342
                      , 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831,
                      1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
                      LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,
                      1520904-1522439); NCI_CGAP_GC4 pool 1     LLAM 3164-3167,
                      3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,
                      1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1
                      LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs
                      985608-986759, 1101192-1101959, 1217928-1220615);
                      NCI_CGAP_Co10 pool 1    LLAM 2644-2653, 2871-2872 (IMAGE
                      CloneIDs 1057416-1061255, 1144584-1145351). Subtraction
                      was performed as previously described [Bonaldo, Lennon &
                      Soares (1996): Normalization and Subtraction: Two
                      Approaches To  Facilitate Gene Discovery. Genome Research
                      6, 791-806.
                      TAG_LIB=NCI_CGAP_Co10
                      TAG_TISSUE=colon
                      TAG_SEQ=AAACG"
BASE COUNT       66 a    132 c    140 g     74 t
ORIGIN

  Query Match             21.0%;  Score 371.4;  DB 10;  Length 412;
  Best Local Similarity   99.5%;  Pred. No. 2.1e-81;
  Matches  383;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy     868 GGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAA 927
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     402 GGCGCCGTGCTTTTGCTCCCCGCGCGCTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAA 343

Qy     928 GCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAAAATGTCAGCTGCTGG 987
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     342 GCCTCGGCCTGCCGCCTTCCACCGTTCATTCTAGAGCAAACAAAAAATGTCAGCTGCTGG 283

Qy     988 CCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCT 1047
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     282 CCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCT 223

Qy    1048 GGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTACTGCCACCGCGAAGAGTT-G 1106
           |||||||||||||||||||||||||||||||||||||| |||||||||||||||||| |
Db     222 GGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCCACTGCCACCGCGAAGAGTTGG 163

Qy    1107 GCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAG 1166
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     162 GCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAG 103

Qy    1167 GAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGCTGTGGGACGTGCAC 1226
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     102 GAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCCCTGAGCTGTGGGACGTGCAC 43

Qy    1227 CCAGGACTCGGCTCACACATGCAGT 1251
           |||||||||||||||||||||||||
Db      42 CCAGGACTCGGCTCACACATGCAGT 18


RESULT 4
AI380754/c
LOCUS       AI380754                376 bp    mRNA    linear   EST 30-MAR-1999
DEFINITION  tf97g05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107256 3',
            mRNA sequence.
ACCESSION   AI380754
VERSION     AI380754.1  GI:4190607
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
```

```
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
            M.D., Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 479   Std Error: 0.00
            Seq primer: -40UP from Gibco.
FEATURES              Location/Qualifiers
     source           1. .376
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2107256"
                      /clone_lib="NCI_CGAP_CLL1"
                      /tissue_type="B-cell, chronic lymphotic leukemia"
                      /lab_host="DH10B"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                      was primed with a Not I - oligo(dT) primer [5'
                      TGTTACCAATCTGAAGTGGGAGCGGCCGCATTGCTTTTTTTTTTTTTTTTTTTTTTT
                      T 3']; double-stranded cDNA was ligated to Eco RI
                      adaptors (Pharmacia), digested with Not I and cloned into
                      the Not I and Eco RI sites of the modified pT7T3 vector.
                      Library is normalized, and was constructed by Bento
                      Soares and M.Fatima Bonaldo."
BASE COUNT       60 a    122 c    133 g     61 t
ORIGIN

  Query Match             20.1%;  Score 355.4;  DB 9;  Length 376;
  Best Local Similarity   99.5%;  Pred. No. 2e-77;
  Matches  367;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy     883 CTCCCCGCGCGCTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGC 942
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 CTCCCCGCGCGCTGTTTTTCTCGCTGACTTTCAGCGGGCGGAAAAGCCTCGGCCTGCCGC 317

Qy     943 CTTCCACCGTTCATTCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCC 1002
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 CTTCCACCGTTCATTCTAGAGCAAACAAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCC 257

Qy    1003 CGGGGACCTGCGGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGG 1062
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     256 CGGGGACCTGCGGCGGGTCGCCTGCCCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGG 197

Qy    1063 CCCGGGGCTTCTCCGGAGGCACCTACTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCG 1121
           |||||||||||||||||||| |||||||||||||||||| ||||||||||||||||||
Db     196 CCCGGGGCTTCTCCGGAGGCACCCACTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCG 137

Qy    1122 GGTCTCTCGGGGGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGC 1181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     136 GGTCTCTCGGGGGCGAGGGCGAGGTTCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGC 77

Qy    1182 GAGTCCCCGCGCGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCA 1241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76 GAGTCCCCGCGCGCGGCGCGATTCCCTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCA 17

Qy    1242 CACATGCAG 1250
           |||||||||
Db      16 CACATGCAG 8


RESULT 5
AW207347/c
LOCUS       AW207347                388 bp    mRNA    linear   EST 02-DEC-1999
DEFINITION  UI-H-BI1-afu-e-09-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone
            IMAGE:2723056 3', mRNA sequence.
ACCESSION   AW207347
VERSION     AW207347.1  GI:6506843
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 388)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a bonafide poly A
            tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            NCI-CGAP clone distribution information can be found through the
            I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html The following repetitive
            elements were found in this cDNA sequence: 286-362,
            >GC_rich#Low_complexity
            Seq primer: M13 Forward
            POLYA=Yes.
FEATURES              Location/Qualifiers
     source           1. .388
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:2723056"
                      /clone_lib="NCI_CGAP_Sub3"
                      /lab_host="DH10B (Life Technologies)"
                      /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                      polylinker; Site_1: Not I; Site_2: Eco RI; The
                      NCI_CGAP_Sub3 library is a subtracted library derived from
                      the NCI_CGAP_Sub1 library, which is a subtracted library
                      derived from BI. BI constitutes a mixture of 21
                      normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4
                      , NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10,
                      NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12,
                      NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2,
                      NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Lei2,
                      NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24,
                      NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,
                      NCI_CGAP_Brn25. These 21 libraries were pooled and a
                      single-stranded DNA preparation of the resulting mixture
                      was used as a tracer in a subtractive hybridization with
                      a driver whose composition is detailed below:
                      NCI_CGAP_Kid3 pool 1    LLAM 3334-3337, 3682-3683,
                      3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775
                      , 1500552-1502855); NCI_CGAP_Kid5 pool 1    LLAM 3338-3342
                      , 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831,
                      1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1
                      LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991,
                      1520904-1522439); NCI_CGAP_GC4 pool 1    LLAM 3164-3167,
                      3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631,
                      1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1
                      LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs
                      985608-986759, 1101192-1101959, 1217928-1220615);
                      NCI_CGAP_Co10 pool 1    LLAM 2644-2653, 2871-2872 (IMAGE
                      CloneIDs 1057416-1061255, 1144584-1145351). Subtraction
                      was performed as previously described [Bonaldo, Lennon &
                      Soares (1996): Normalization and Subtraction: Two
                      Approaches To Facilitate Gene Discovery. Genome Research
                      6, 791-806.
                      TAG_LIB=NCI_CGAP_Co10
                      TAG_TISSUE=colon
                      TAG_SEQ=AAACG"
BASE COUNT       58 a    127 c    132 g     71 t
ORIGIN

  Query Match             20.1%;  Score 355.2;  DB 10;  Length 388;
  Best Local Similarity   98.9%;  Pred. No. 2.2e-77;
  Matches  368;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy     968 CAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGC 1027
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 CAAAAAATGTCAGCTGCTGGCCCGTTCGCCCCTCCCGGGGACCTGCGGCGGGTCGCCTGC 329

Qy   1028 CCAGCCCCCGAACCCCGCCTGGAGGCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCTA 1087
          |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||| |
Db    328 CCAGCCCCCGAACCCCGCCTGGAGCCCGCGGTCGGCCCGGGGCTTCTCCGGAGGCACCCA 269

Qy   1088 CTGCCACCGCGAAGAGTT-GGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGT 1146
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db    268 CTGCCACCGCGAAGAGTTGGGCTCTGTCAGCCGCGGGTCTCTCGGGGGCGAGGGCGAGGT 209

Qy   1147 TCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCC 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 TCAGGCCTTTCAGGCCGCAGGAAGAGGAACGGAGCGAGTCCCCGCGCGCGGCGCGATTCC 149

Qy   1207 CTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGG 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 CTGAGCTGTGGGACGTGCACCCAGGACTCGGCTCACACATGCAGTTCGCTTTCCTGTTGG 89

Qy   1267 TGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAGTGGGGGCTTGTGAAC 1326
          |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     88 TGGGGGGAACGCCGATCGTGCGCATCCGTCACCCCTCGCCGGCAATGGGGGCTTGTGAAC 29

Qy   1327 CCCCAAACCTGA 1338
          ||||||||||||
Db     28 CCCCAAACCTGA 17
```

RESULT 6
BM695101/c

```
LOCUS       BM695101                353 bp    mRNA    linear   EST 28-FEB-2002
DEFINITION  UI-E-CL1-aez-h-03-0-UI.r1 UI-E-CL1 Homo sapiens cDNA clone
            UI-E-CL1-aez-h-03-0-UI 5', mRNA sequence.
ACCESSION   BM695101
VERSION     BM695101.1  GI:19008359
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 353)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .353
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-E-CL1-aez-h-03-0-UI"
                     /clone_lib="UI-E-CL1"
                     /tissue_type="human retina"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-CL1 is a normalized cDNA library containing the
                     following tissue(s): retina. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CCGCG. This library was
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI)."
BASE COUNT      111 a     88 c     74 g     80 t
ORIGIN
```

```
  Query Match             19.9%;  Score 351.4;  DB 14;  Length 353;
  Best Local Similarity   99.7%;  Pred. No. 1.9e-76;
  Matches  352;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1323 GAACCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGC 1382
          || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    353 GAGCCCCCAAACCTGACTGACTGGGCCAGTGTGCTGCAAATTGGCAGGAGACGTGAAGGC 294

Qy   1383 ACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTG 1442
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    293 ACCTCCAAAGTCGGCCAAAATGAATGGGCAGTGAGCCGGGGTTGCCTGGAGCCGTTCCTG 234

Qy   1443 CGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTC 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    233 CGTGGGTTCTCCCGTCTTCCGCTTTTTGTTGCCTTTTATGGTTGTATTACAACTTAGTTC 174

Qy   1503 CTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCC 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    173 CTGCTCTGCAGATTTTGTTGAGGTTTTTGCTTCTCCCAAGGTAGATCTCGACCAGTCCCC 114

Qy   1563 TCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAAT 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    113 TCAACGGGGTGTGGGAGAACAGTCATTTTTTTTTGAGAGATCATTTAACATTTAATGAAT 54

Qy   1623 ATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCA 1675
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     53 ATTTAATTAGAAGATCTAAATGAACATTGGAAATTGTGTTCCTTTAATGGTCA 1
```

RESULT 7
AQ229478/c

```
LOCUS       AQ229478                466 bp    DNA     linear   GSS 26-SEP-1998
DEFINITION  HS_2021_A2_A08_MR CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=2021 Col=16 Row=A, DNA sequence.
ACCESSION   AQ229478
VERSION     AQ229478.1  GI:3654707
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 466)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Sequence Tagged Connector
            Plate: 2021  row: A  column: 16
            Class: BAC ends
```

```
          High quality sequence stop: 466.
FEATURES             Location/Qualifiers
     source          1. .466
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="Plate=2021 Col=16 Row=A"
                     /clone_lib="CIT Approved Human Genomic Sperm Library D"
                     /sex="male"
                     /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                     E-Coli DH10B"
BASE COUNT       113 a     94 c    111 g    147 t      1 others
ORIGIN

  Query Match             6.3%;  Score 110.8;  DB 17;  Length 466;
  Best Local Similarity   90.8%;  Pred. No. 1.1e-16;
  Matches  118;  Conservative    0;  Mismatches   12;  Indels    0;  Gaps    0;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           |||||||||||||||||| || ||||||| |||||||| |||||| ||||||||||||
Db     399 AGCTACTCAGGAGGCTGAGGCAGGAGAATCACTTGAACCCAGGAGGCGGAGGTTGCAGTG 340

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           |||| |||||||||||  |  |||||||||||| |||| || ||||||||||||||||||
Db     339 AGCCAAGATCACGCCAGTGCACTCCATCCAGCATGGGAGACAGAGCAAGACTCCGTCTCA 280

Qy     121 AAAAAAAAAA 130
           ||||||||||
Db     279 AAAAAAAAAA 270


RESULT 8
AG186502
LOCUS       AG186502                680 bp    DNA     linear   GSS 09-JAN-2002
DEFINITION  Pan troglodytes DNA, clone: RP43-060015.T7, genomic survey
            sequence.
ACCESSION   AG186502
VERSION     AG186502.1  GI:16716182
KEYWORDS    GSS.
SOURCE      Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
            Male BAC Library clone:RP43-060015.T7.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library RPCI-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 680)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: T7
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .680
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="RP43-060015.T7"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT       194 a    156 c    163 g    121 t     46 others
ORIGIN

  Query Match             6.2%;  Score 109.2;  DB 17;  Length 680;
  Best Local Similarity   87.0%;  Pred. No. 2.9e-16;
  Matches  120;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           |||||||| ||||||||||  | |||||| |||||||| | ||||||||||||||||||||
Db     239 AGCTACTCGGGAGGCTGAGGAAAGAGAATTGCTTGAACTCAGGAGGCAGAGGTTGCAGTG 298

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           |||||||||| ||||||  ||||||| |||||||||||| |||||||||||||||||| |
Db     299 AGCCGAGATCATGCCACTGCACTCCATTCAGCCTGGGCGACAGAGCAAGACTCCGTCTGA 358

Qy     121 AAAAAAAAAATCGTTACA 138
           ||||||||||  |  | |
Db     359 AAAAAAAAAAAAGAAAAA 376


RESULT 9
AQ390169
LOCUS       AQ390169                418 bp    DNA     linear   GSS 06-MAR-1999
DEFINITION  CITBI-E1-2544A19.TF CITBI-E1 Homo sapiens genomic clone 2544A19,
            DNA sequence.
ACCESSION   AQ390169
VERSION     AQ390169.1  GI:4361192
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 418)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2544A19.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .418
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="2544A19"
                     /clone_lib="CITBI-E1"
                     /sex="male"
                     /cell_type="sperm"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
BASE COUNT       132 a    109 c    104 g     73 t
ORIGIN

  Query Match             6.1%;  Score 107.6;  DB 17;  Length 418;
  Best Local Similarity   86.2%;  Pred. No. 6.8e-16;
  Matches  119;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           |||| |    |||||||| || | ||||| ||||||||||||||||||||||| |||||
Db      95 AGCTGCCTGAGAGGCTGAGGCATGGGAATCACTTGAACCCGGGAGGCAGAGGTTACAGTG 154
```

```
Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||||||||||||||||  |||||||||||||| ||| | ||||||||||||||||||
Db     155 AGCCGAGATCACGCCACTGCACTCCATCCAGCCTAGGCAACAGAGCAAGACTCCGTCTCA 214

Qy     121 AAAAAAAAAATCGTTACA 138
           |||||||||| |   |||
Db     215 AAAAAAAAAAACAAAACA 232


RESULT 10
BM509394
LOCUS       BM509394                469 bp    mRNA    linear   EST 15-FEB-2002
DEFINITION  ih17f10.y1 Human insulinoma Homo sapiens cDNA 5' similar to
            SW:ALU8_HUMAN P39195 ALU SUBFAMILY SX SEQUENCE CONTAMINATION
            WARNING ENTRY. [1] ;, mRNA sequence.
ACCESSION   BM509394
VERSION     BM509394.1  GI:18680537
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 469)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
            , Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 416.
FEATURES             Location/Qualifiers
     source          1. .469
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="Human insulinoma"
                     /tissue_type="insulinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Hiroshi Inoue, MD/PhD for further
                     information on this library (Metabolism Division, Permutt
                     Laboratory, Washington University School of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                     is a Washington University Pancreas EST project library. "
BASE COUNT      149 a     93 c     94 g    133 t
ORIGIN

  Query Match             6.1%;  Score 107.2;  DB 13;  Length 469;
  Best Local Similarity   81.6%;  Pred. No. 8.6e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           ||| |||| ||||||| | |   ||||||||||||||||| ||||||||||||||||||
Db     285 AGCCACTCGGGAGGCTTAAATGGGAGAATCGCTTGAACCCTGGAGGCAGAGGTTGCAGTG 344

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||  || |||||||||  |||||||||||||||| || ||||||||||||| |||||
Db     345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
           ||||||||||  | |   |   ||| ||  ||
Db     405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 11
BI468297
LOCUS       BI468297                516 bp    mRNA    linear   EST 11-MAR-2002
DEFINITION  id87b01.y1 Human insulinoma Homo sapiens cDNA clone IMAGE:5022649
            5', mRNA sequence.
ACCESSION   BI468297
VERSION     BI468297.1  GI:15284406
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 516)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
            , Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            High quality sequence stop: 457.
FEATURES             Location/Qualifiers
     source          1. .516
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5022649"
                     /clone_lib="Human insulinoma"
                     /tissue_type="insulinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Hiroshi Inoue, MD/PhD for further
                     information on this library (Metabolism Division, Permutt
                     Laboratory, Washington University School of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                     is a Washington University Pancreas EST project library. "
BASE COUNT      157 a    103 c    104 g    152 t
ORIGIN

  Query Match             6.1%;  Score 107.2;  DB 13;  Length 516;
  Best Local Similarity   81.6%;  Pred. No. 8.7e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           ||| |||| ||||||| | |   ||||||||||||||||| ||||||||||||||||||
Db     285 AGCCACTCGGGAGGCTTAAATGGGAGAATCGCTTGAACCCTGGAGGCAGAGGTTGCAGTG 344
```

```
Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||  || |||||||||  |||||||||||||||||| || |||||||||||| |||||
Db     345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
           ||||||||||  | |   |   ||| ||  ||
Db     405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 12
BQ270800
LOCUS       BQ270800                529 bp    mRNA    linear   EST 07-MAY-2002
DEFINITION  ik05b06.y1 Human insulinoma Homo sapiens cDNA clone IMAGE: 5779930
            5', mRNA sequence.
ACCESSION   BQ270800
VERSION     BQ270800.1  GI:20495866
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 529)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
            , Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: ik05b06.x1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 428.
FEATURES             Location/Qualifiers
     source          1. .529
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE: 5779930"
                     /clone_lib="Human insulinoma"
                     /tissue_type="insulinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue  following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact  Hiroshi Inoue, MD/PhD for further
                     information on this library  (Metabolism Division, Permutt
                     Laboratory, Washington University School  of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110).  Note: this
                     is a Washington University Pancreas EST project library. "
BASE COUNT      160 a    107 c    107 g    155 t
ORIGIN

  Query Match             6.1%;  Score 107.2;  DB 14;  Length 529;
  Best Local Similarity   81.6%;  Pred. No. 8.7e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;

Qy      1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
```

```
           ||| |||| ||||||| | |   |||||||||||||||| ||||||||||||||||||
Db     285 AGCCACTCGGGAGGCTTAAATGGGAGAATCGCTTGAACCCTGGAGGCAGAGGTTGCAGTG 344

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||  || |||||||||  |||||||||||||||||| || |||||||||||| |||||
Db     345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
           ||||||||||  | |   |   ||| ||  ||
Db     405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 13
BQ267333
LOCUS       BQ267333                556 bp    mRNA    linear   EST 07-MAY-2002
DEFINITION  ik02c03.y1 Human insulinoma Homo sapiens cDNA clone IMAGE: 5779589
            5', mRNA sequence.
ACCESSION   BQ267333
VERSION     BQ267333.1  GI:20492398
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 556)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
            , Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 428.
FEATURES             Location/Qualifiers
     source          1. .556
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE: 5779589"
                     /clone_lib="Human insulinoma"
                     /tissue_type="insulinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue  following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact  Hiroshi Inoue, MD/PhD for further
                     information on this library  (Metabolism Division, Permutt
                     Laboratory, Washington University School  of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110).  Note: this
                     is a Washington University Pancreas EST project library. "
BASE COUNT      167 a    112 c    113 g    164 t
ORIGIN

  Query Match             6.1%;  Score 107.2;  DB 14;  Length 556;
  Best Local Similarity   81.6%;  Pred. No. 8.8e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;
```

```
Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           ||| |||| ||||||| | |   ||||||||||||||||| ||||||||||||||||||
Db     285 AGCCACTCGGGAGGCTTAAATGGGAGAATCGCTTGAACCCTGGAGGCAGAGGTTGCAGTG 344

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||  || |||||||||  |||||||||||||||| || ||||||||||||| |||||
Db     345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
           ||||||||||  | |   |   ||| ||  ||
Db     405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 14
BQ270346
LOCUS       BQ270346                589 bp    mRNA    linear   EST 07-MAY-2002
DEFINITION  ik09g10.y1 Human insulinoma Homo sapiens cDNA clone IMAGE: 5780562
            5', mRNA sequence.
ACCESSION   BQ270346
VERSION     BQ270346.1  GI:20495412
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas
            ,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T.
            , Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. J. Ferrer In vivo mass-excised to
            pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington
            University Genome Sequencing Center For information on obtaining a
            clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
            Seq primer: -40RP from Gibco
            High quality sequence stop: 427.
FEATURES             Location/Qualifiers
     source          1. .589
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE: 5780562"
                     /clone_lib="Human insulinoma"
                     /tissue_type="insulinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
                     XhoI; Site_2: EcoRI; Constructed with lambda ZAPII system
                     (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
                     pBluescript SK- by Dr. H. Inoue following the Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Hiroshi Inoue, MD/PhD for further
                     information on this library (Metabolism Division, Permutt
                     Laboratory, Washington University School of Medicine, Box
                     8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
                     is a Washington University Pancreas EST project library. "
BASE COUNT      177 a    122 c    116 g    174 t
ORIGIN

  Query Match             6.1%;  Score 107.2;  DB 14;  Length 589;
  Best Local Similarity   81.6%;  Pred. No. 8.8e-16;
  Matches  124;  Conservative    0;  Mismatches   28;  Indels    0;  Gaps    0;
```

```
Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           ||| |||| ||||||| | |   ||||||||||||||||| ||||||||||||||||||
Db     285 AGCCACTCGGGAGGCTTAAATGGGAGAATCGCTTGAACCCTGGAGGCAGAGGTTGCAGTG 344

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||  || |||||||||  |||||||||||||||| || ||||||||||||| |||||
Db     345 AGCCAGGACCACGCCACTGCACTCCATCCAGCCTGGGTGACAGAGCAAGACTCCATCTCA 404

Qy     121 AAAAAAAAAATCGTTACAATTTATGGTGGATT 152
           ||||||||||  | |   |   ||| ||  ||
Db     405 AAAAAAAAAAAAGGTTAGAAAAATGCTGCTTT 436


RESULT 15
AQ428429
LOCUS       AQ428429                635 bp    DNA     linear   GSS 24-MAR-1999
DEFINITION  CITBI-E1-2564J3.TF CITBI-E1 Homo sapiens genomic clone 2564J3, DNA
            sequence.
ACCESSION   AQ428429
VERSION     AQ428429.1  GI:4496195
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 635)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2564J3.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .635
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="2564J3"
                     /clone_lib="CITBI-E1"
                     /sex="male"
                     /cell_type="sperm"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
BASE COUNT      218 a    129 c    119 g    169 t
ORIGIN

  Query Match             6.0%;  Score 106.4;  DB 17;  Length 635;
  Best Local Similarity   67.3%;  Pred. No. 1.4e-15;
  Matches  167;  Conservative    0;  Mismatches   76;  Indels    5;  Gaps    1;

Qy       1 AGCTACTCAGGAGGCTGAGACACGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTG 60
           ||||| ||||||| ||||| || ||||||| ||||||||||||||  |||||| ||||
Db     307 AGCTATTCAGGAGCCTGAGGCAGGAGAATCACTTGAACCCGGGAGGTGGAGGTTACAGTG 366

Qy      61 AGCCGAGATCACGCCACTAGACTCCATCCAGCCTGGGCGAAAGAGCAAGACTCCGTCTCA 120
           ||||||||||| |||||||  ||||||||||||||||  || ||||  |||||||  ||||
Db     367 AGCCGAGATCGCGCCACTGCACTCCATCCAGCCTGGCAGACAGAGTGAGACTCCAGCTCA 426

Qy     121 AAAAAAAAAATCGTTACAAT-----TTATGGTGGATTACTCCCCTCTTTTTACCTCATCA 175
           ||||||||||     | |||     ||      ||| || | | |  || | |  |  |
Db     427 AAAAAAAAAAAAAAAAAAAATTCCACTTTAAACTGATACCTACACCCAGTTGATCAGACAA 486
```

```
Qy     176 AGACACAGCACTACTTTAAAGCAAAGTCAATGATTGAAACGCCTTTCTTTCCTAATAAAA 235
           |    ||| | ||   ||||  ||| | |    ||   | |  ||  |||  |||||| |
Db     487 ACTAGCAGGAGTAAGATAAACTTAATTTATGATTTACCAAGTATTAATTTGATAATAATA 546

Qy     236 GGGAGATT 243
             || | |
Db     547 TAGACAGT 554
```

Search completed: December 19, 2002, 14:46:57
Job time : 2153 secs